



results of BLAST

BLASTP 2.2.14 [May-07-2006]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference:

Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005.

RID: 1153506756-5678-199370517911.BLASTQ4

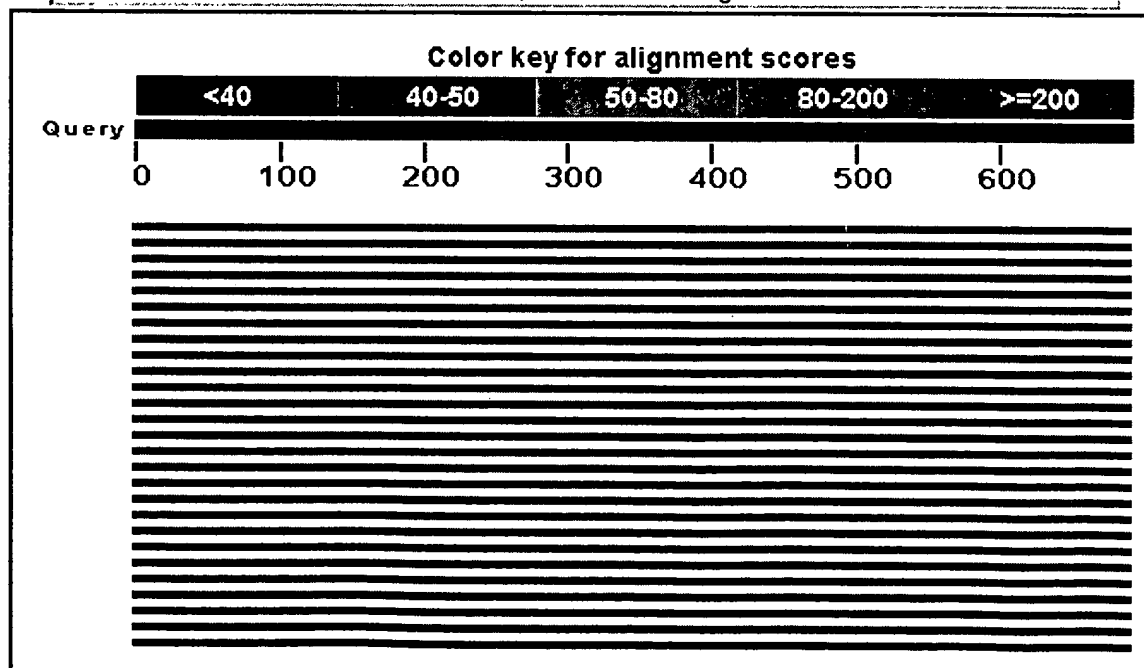
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples
3,805,897 sequences; 1,312,134,661 total letters

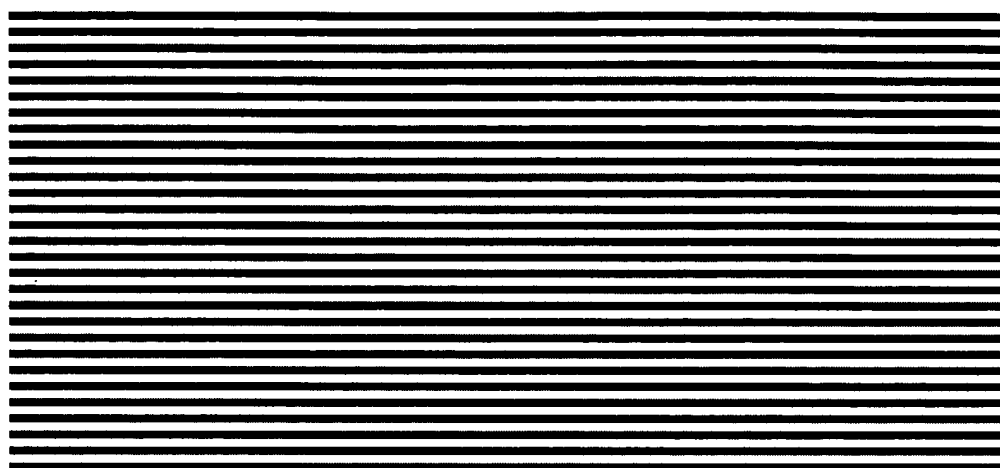
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=685

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments





[Distance tree of results](#) [NEW](#) [Related Structures](#)

Sequences producing significant alignments:		Score (Bits)	E Value
gi 130455 sp P26664 POLG HCV1	Genome polyprotein [Contains: C...	1302	0.0
gi 14532249 gb AAK66556.1 	HCV type 1a/1b chimera polyprotein...	1302	0.0
gi 8926245 gb AAF81759.1 	polyprotein [Hepatitis C virus]	1301	0.0
gi 14532251 gb AAK66557.1 	HCV type 1a/1b chimera mutant polypro	1299	0.0
gi 329876 gb AAA45677.1 	polyprotein	1297	0.0
gi 63079188 gb AAY29640.1 	polyprotein [Hepatitis C virus]	1287	0.0
gi 55275808 gb AAV49742.1 	polyprotein [Hepatitis C virus]	1286	0.0
gi 48479030 gb AAT44836.1 	polyprotein [Hepatitis C virus]	1286	0.0
gi 22129793 ref NP_671491.1 	polyprotein [Hepatitis C virus] ...	1286	0.0
gi 6010588 gb AAF01182.1 	polyprotein [synthetic construct] >...	1285	0.0
gi 6010586 gb AAF01181.1 	polyprotein [synthetic construct] >...	1285	0.0
gi 9930557 gb AAG02099.1 	polyprotein [Hepatitis C virus]	1284	0.0
gi 2327071 gb AAB67036.1 	polyprotein [Hepatitis C virus strain	1283	0.0
gi 63079190 gb AAY29641.1 	polyprotein [Hepatitis C virus]	1283	0.0
gi 55275810 gb AAV49743.1 	polyprotein [Hepatitis C virus]	1282	0.0
gi 63079194 gb AAY29643.1 	polyprotein [Hepatitis C virus]	1281	0.0
gi 2327075 gb AAB67038.1 	polyprotein [Hepatitis C virus strain	1280	0.0
gi 9843677 emb CAC03609.1 	unnamed protein product [Hepatitis C	1278	0.0
gi 221587 dbj BAA01582.1 	polyprotein precursor [Hepatitis C vir	1278	0.0
gi 63079186 gb AAY29639.1 	polyprotein [Hepatitis C virus]	1278	0.0
gi 2327073 gb AAB67037.1 	polyprotein [Hepatitis C virus strain	1278	0.0
gi 63079196 gb AAY29644.1 	polyprotein [Hepatitis C virus]	1275	0.0
gi 130461 sp P27958 POLG HCVH	Genome polyprotein [Contains: C...	1268	0.0
gi 63079184 gb AAY29638.1 	polyprotein [Hepatitis C virus]	1263	0.0
gi 7650260 gb AAF65961.1 	polyprotein [Hepatitis C virus]	1234	0.0
gi 11559457 dbj BAB18808.1 	polyprotein [Hepatitis C virus]	1234	0.0
gi 7650232 gb AAF65947.1 	polyprotein [Hepatitis C virus]	1233	0.0
gi 5918947 gb AAD56189.1 	polyprotein [Hepatitis C virus]	1233	0.0
gi 5918965 gb AAD56198.1 	polyprotein [Hepatitis C virus]	1232	0.0
gi 130458 sp P26663 POLG HCVBK	Genome polyprotein [Contains: ...	1232	0.0
gi 12831193 gb AAK08509.1 	polyprotein [Hepatitis C virus type 1	1232	0.0
gi 7650246 gb AAF65954.1 	polyprotein [Hepatitis C virus]	1232	0.0
gi 5918945 gb AAD56188.1 	polyprotein [Hepatitis C virus]	1232	0.0
gi 7650244 gb AAF65953.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 5918939 gb AAD56185.1 	polyprotein [Hepatitis C virus]	1231	0.0
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gi 46560636 gb AAT00644.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 23957857 gb AAD44718.2 	polyprotein [Hepatitis C virus]	1231	0.0
gi 7650266 gb AAF65964.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 5821155 dbj BAA83719.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 87080431 emb CAH64686.1 	polyprotein [Hepatitis C virus]	1231	0.0
gi 5918967 gb AAD56199.1 	polyprotein [Hepatitis C virus]	1230	0.0
gi 11559469 dbj BAB18814.1 	polyprotein [Hepatitis C virus]	1230	0.0
gi 48237634 gb AAT40682.1 	polyprotein [Hepatitis C virus]	1230	0.0
gi 1212742 dbj BAA08120.1 	HCV polyprotein [Hepatitis C virus]	1230	0.0
gi 7650248 gb AAF65955.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 7650236 gb AAF65949.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 5918951 gb AAD56191.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 266820 sp Q00269 POLG HCVJT	Genome polyprotein [Contains: ...	1229	0.0
gi 464178 dbj BAA03581.1 	polyprotein [Hepatitis C virus (iso...	1229	0.0
gi 11559447 dbj BAB18803.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 5918949 gb AAD56190.1 	polyprotein [Hepatitis C virus]	1229	0.0
gi 5441839 emb CAB46915.1 	non-structural polyprotein [Hepati...	1229	0.0
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gi 7650228 gb AAF65945.1 	polyprotein [Hepatitis C virus]	1228	0.0
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gi 7650256 gb AAF65959.1 	polyprotein [Hepatitis C virus]	1228	0.0
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gi 46560634 gb AAT00643.1 	polyprotein [Hepatitis C virus]	1227	0.0
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gi 11559445 dbj BAB18802.1 	polyprotein [Hepatitis C virus]	1227	0.0
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gi 5918931 gb AAD56181.1 	polyprotein [Hepatitis C virus]	1226	0.0
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gi 5918935 gb AAD56183.1 	polyprotein [Hepatitis C virus]	1221	0.0
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gi 5918963 gb AAD56197.1 	polyprotein [Hepatitis C virus]	1216	0.0
gi 5918961 gb AAD56196.1 	polyprotein [Hepatitis C virus]	1216	0.0
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gi 3098639 qb AAC15725.1 	polyprotein [Hepatitis C virus]	1213	0.0
gi 1814090 dbj BAA09075.1 	polyprotein [Hepatitis C virus]	1212	0.0
gi 56342207 dbj BAD73981.1 	polyprotein [Hepatitis C virus type	1212	0.0
gi 3098646 qb AAC15728.1 	polyprotein [Hepatitis C virus]	1212	0.0
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gi 3098653 qb AAC15731.1 	polyprotein [Hepatitis C virus]	1211	0.0
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gi 3098655 qb AAC15732.1 	polyprotein [Hepatitis C virus]	1210	0.0
gi 80322850 qb ABB52627.1 	polyprotein [Hepatitis C virus]	1209	0.0
gi 2943784 dbj BAA25076.1 	polyprotein [Hepatitis C virus]	1207	0.0
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gi 306287 qb AAA45721.1 	putative	1199	0.0
gi 50235322 qb AAT69968.1 	polyprotein [Hepatitis C virus]	1199	0.0
gi 567060 qb AAA52748.1 	polyprotein	1198	0.0
gi 5748511 emb CAB53095.1 	polyprotein [Hepatitis C virus type 1	1197	0.0
gi 437108 qb AAA75355.1 	polyprotein	1197	0.0
gi 7650258 qb AAF65960.1 	polyprotein [Hepatitis C virus]	1195	0.0
gi 4753721 emb CAB41951.1 	polyprotein [Hepatitis C virus]	1193	0.0
gi 7650262 qb AAF65962.1 	polyprotein [Hepatitis C virus]	1193	0.0
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gi 67810846 qb AAY82011.1 	polyprotein [Hepatitis C virus]	1174	0.0
gi 67810857 qb AAY82016.1 	polyprotein [Hepatitis C virus]	1172	0.0
gi 67810849 qb AAY82012.1 	polyprotein [Hepatitis C virus]	1172	0.0
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gi 67810879 qb AAY82026.1 	polyprotein [Hepatitis C virus]	1170	0.0
gi 67810877 qb AAY82025.1 	polyprotein [Hepatitis C virus]	1170	0.0
gi 67810842 qb AAY82009.1 	polyprotein [Hepatitis C virus]	1170	0.0
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gi 67810855 qb AAY82015.1 	polyprotein [Hepatitis C virus]	1169	0.0
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gi 67810868 qb AAY82021.1 	polyprotein [Hepatitis C virus]	1168	0.0
gi 67810883 qb AAY82028.1 	polyprotein [Hepatitis C virus]	1167	0.0
gi 28921568 ref NP_803144.1 	NS3 protease/helicase' [Hepatitis C	1167	0.0
gi 67810881 qb AAY82027.1 	polyprotein [Hepatitis C virus]	1167	0.0
gi 67810887 qb AAY82030.1 	polyprotein [Hepatitis C virus]	1167	0.0
gi 67810844 qb AAY82010.1 	polyprotein [Hepatitis C virus]	1166	0.0
gi 67810870 qb AAY82022.1 	polyprotein [Hepatitis C virus]	1165	0.0
gi 67810851 qb AAY82013.1 	polyprotein [Hepatitis C virus]	1165	0.0
gi 67810896 qb AAY82034.1 	polyprotein [Hepatitis C virus]	1164	0.0
gi 67810861 qb AAY82018.1 	polyprotein [Hepatitis C virus]	1163	0.0
gi 67810894 qb AAY82033.1 	polyprotein [Hepatitis C virus]	1162	0.0
gi 67810864 qb AAY82019.1 	polyprotein [Hepatitis C virus]	1162	0.0
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gi 68012736 qb AAY84764.1 	nonstructural protein 3 [Hepatitis...	1161	0.0
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gi 68012748 qb AAY84770.1 	nonstructural protein 3 [Hepatitis C	1160	0.0
gi 68012732 qb AAY84762.1 	nonstructural protein 3 [Hepatitis C	1160	0.0
gi 68012726 qb AAY84759.1 	nonstructural protein 3 [Hepatitis C	1160	0.0
gi 68012712 qb AAY84752.1 	nonstructural protein 3 [Hepatitis C	1159	0.0
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gi 68012708 qb AAY84750.1 	nonstructural protein 3 [Hepatitis C	1159	0.0
gi 68012698 qb AAY84745.1 	nonstructural protein 3 [Hepatitis C	1159	0.0

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gi 68012714 qb AAAY84753.1 	nonstructural protein 3 [Hepatitis C	1158	0.0
gi 68012746 qb AAAY84769.1 	nonstructural protein 3 [Hepatitis C	1158	0.0
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gi 68012722 qb AAAY84757.1 	nonstructural protein 3 [Hepatitis C	1156	0.0
gi 68012740 qb AAAY84766.1 	nonstructural protein 3 [Hepatitis C	1155	0.0
gi 89519405 qb ABD75824.1 	polyprotein [Hepatitis C virus]	1155	0.0
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gi 67810885 qb AAAY82029.1 	polyprotein [Hepatitis C virus]	1152	0.0
gi 89519413 qb ABD75828.1 	polyprotein [Hepatitis C virus]	1151	0.0
gi 89519407 qb ABD75825.1 	polyprotein [Hepatitis C virus]	1151	0.0
gi 89519415 qb ABD75829.1 	polyprotein [Hepatitis C virus]	1150	0.0
gi 89519411 qb ABD75827.1 	polyprotein [Hepatitis C virus]	1150	0.0
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gi 73765377 qb AAZ85046.1 	polyprotein [Hepatitis C virus]	1145	0.0
gi 93102510 qb ABE98157.1 	polyprotein [Hepatitis C virus subtyp	1145	0.0
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gi 93102494 qb ABE98149.1 	polyprotein [Hepatitis C virus subtyp	1142	0.0
gi 81985682 sp Q5I2N3 POLG	HCV6A Genome polyprotein [Contains...	1142	0.0
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gi 93102502 qb ABE98153.1 	polyprotein [Hepatitis C virus subtyp	1140	0.0
gi 93102514 qb ABE98159.1 	polyprotein [Hepatitis C virus subtyp	1139	0.0
gi 93102496 qb ABE98150.1 	polyprotein [Hepatitis C virus subtyp	1139	0.0
gi 93102512 qb ABE98158.1 	polyprotein [Hepatitis C virus subtyp	1138	0.0
gi 93102508 qb ABE98156.1 	polyprotein [Hepatitis C virus subtyp	1138	0.0
gi 469213 dbj BAA05975.1 	fusion protein, composed of HCV p21...	1137	0.0
gi 93102516 qb ABE98160.1 	polyprotein [Hepatitis C virus subtyp	1134	0.0
gi 3550761 dbj BAA32665.1 	polyprotein [Hepatitis C virus (is...	1134	0.0
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gi 62362180 qb AAX81527.1 	polyprotein [Hepatitis C virus]	1130	0.0
gi 82617874 qb ABB84854.1 	polyprotein precursor [Hepatitis C vi	1130	0.0
gi 82617878 qb ABB84856.1 	polyprotein precursor [Hepatitis C vi	1129	0.0
gi 82617876 qb ABB84855.1 	polyprotein precursor [Hepatitis C vi	1129	0.0
gi 81921385 sp O39928 POLG	HCVEV Genome polyprotein [Contains...	1127	0.0
gi 81921384 sp O39927 POLG	HCVEU Genome polyprotein [Contains...	1122	0.0
gi 3550765 dbj BAA32667.1 	polyprotein [Hepatitis C virus (is...	1121	0.0
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gi 67810990 qb AAAY82045.1 	polyprotein [Hepatitis C virus]	1119	0.0
gi 67810986 qb AAAY82043.1 	polyprotein [Hepatitis C virus]	1119	0.0
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gi 67811012 qb AAAY82056.1 	polyprotein [Hepatitis C virus]	1117	0.0

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gi 67811004 gb AAY82052.1 	polyprotein [Hepatitis C virus]	1116	0.0
gi 89113921 gb AAV75597.2 	polyprotein precursor [Hepatitis C vi	1116	0.0
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gi 67811026 gb AAY82063.1 	polyprotein [Hepatitis C virus]	1113	0.0
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gi 33413949 gb AAP55700.1 	polyprotein [Hepatitis C virus]	1069	0.0
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gi 5616215 gb AAD45674.1	NS3 helicase [Hepatitis C virus]	814	0.0	
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gi 5031420 gb AAD38162.1	polyprotein [Hepatitis C virus]	811	0.0	
gi 5616212 gb AAD45673.1	NS3 helicase [Hepatitis C virus]	808	0.0	
gi 1372955 gb AAB02124.1	NS3 gene product	808	0.0	
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gi 83755049 pdb 2F55 C Chain C, Two Hepatitis C Virus Ns3 Hel...		794	0.0	S
gi 4930270 pdb 8OHM Crystal Structure Of Rna Helicase From ...		787	0.0	S
gi 793912 gb AAA65789.1	precursor protein	708	0.0	
gi 221620 dbj BAA03177.1	NS3-4 protein [Hepatitis C virus]	699	0.0	
gi 5353561 gb AAD42179.1	superoxide dismutase/HCV major epit...	535	2e-150	
gi 2731650 gb AAB93501.1	polyprotein [Hepatitis C virus]	519	2e-145	
gi 2731652 gb AAB93502.1	polyprotein [Hepatitis C virus]	502	2e-140	
gi 765334 gb AAB31751.1	c33-c antigen [Hepatitis C virus]	496	1e-138	
gi 221622 dbj BAA03178.1	NS3 protein [Hepatitis C virus]	488	5e-136	
gi 2160336 dbj BAA01515.1	ORF 1 [Hepatitis C virus]	484	7e-135	
gi 4433101 dbj BAA20994.1	NS3 protein [Hepatitis C virus]	472	2e-131	
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gi 2660983 gb AAB88168.1	polyprotein [Hepatitis C virus]	459	2e-127	

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gi 2660935 gb AAB88144.1 	polyprotein [Hepatitis C virus]	456	2e-126
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gi 2660975 gb AAB88164.1 	polyprotein [Hepatitis C virus]	444	7e-123
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gi 3157754 dbj BAA28505.1 	polyprotein [Hepatitis C virus]	403	2e-110
gi 3157740 dbj BAA28498.1 	polyprotein [Hepatitis C virus]	402	4e-110
gi 3157742 dbj BAA28499.1 	polyprotein [Hepatitis C virus]	401	5e-110
gi 3157748 dbj BAA28502.1 	polyprotein [Hepatitis C virus]	400	1e-109
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gi 33090378 gb AAP57528.1 	polyprotein [synthetic construct]	400	1e-109
gi 13162188 emb CAC33083.1 	polyprotein [Hepatitis GB virus B]	400	2e-109
gi 9628102 ref NP_056931.1 	polyprotein [Hepatitis GB virus B...	400	2e-109
gi 21727887 emb CAD21957.1 	non-structural polyprotein [Hepatiti	397	8e-109
gi 3157802 dbj BAA28529.1 	polyprotein [Hepatitis C virus] >g...	396	2e-108

Alignments

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Deselect all

Distance tree of results

> [gi|130455|sp|P26664|POLG_HCV1](#) Genome polyprotein [Contains: Core protein p21 (Caps: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|329874|gb|AAA45676.1|](#) HCV-1
Length=3011

Score = 1302 bits (3370), Expect = 0.0, Method: Composition-based stats.
Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLYREFDEMEEC	1711

> gi|14532249|gb|AAK66556.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
gi|14532247|gb|AAK66555.1| HCV type 1a polyprotein [synthetic construct]
gi|14532245|gb|AAK66554.1| HCV type 1a/1b chimera polyprotein [synthetic construct]
 Length=3011

Score = 1302 bits (3370), Expect = 0.0, Method: Composition-based stats.
 Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWVlvvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLYREFDEMEEC	1711

> [gi|8926245|gb|AAF81759.1|](#) polyprotein [Hepatitis C virus]
Length=3011

Score = 1301 bits (3366), Expect = 0.0, Method: Composition-based stats.
Identities = 682/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240

Sbjct	1207	SPVF T DNSSPPVVPQSFQVAHLHAPTGS G SKTKVPAA Y AAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY G KFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY G KFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPG S VTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPG S VTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELA A AKLVALGINAVAYYRGLDVSVIPGDV V VVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA A AKLVALGINAVAYYRGLDVSVIPGDV V VVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD F SLDPTFTT I ETITL P QDAVSrtqrrgrtg r gKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD F SLDPTFTT I ETITL P QDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT P GLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT P GLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvgg v laalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	VLSGKPAIIPDREVLY+EFDEMEEC 1711	

> gi|14532251|gb|AAK66557.1| HCV type 1a/1b chimera mutant polyprotein [synthetic cor
Length=3011

Score = 1299 bits (3362), Expect = 0.0, Method: Composition-based stats.
Identities = 681/685 (99%), Positives = 682/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGS R SLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGS R SLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLC P AGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKGSSGGPLLC P AGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVF T DNSSPPVVPQSFQVAHLHAPTGS G +TKVPAA Y AAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVF T DNSSPPVVPQSFQVAHLHAPTGS G AATKVPAA Y AAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY G KFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY G KFLADGGCSGGAYDIIICDECHSTDATSI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVSLDPTFTIETITLPPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVSLDPTFTIETITLPPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVSLDPTFTIETITLPPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKPAIIPDREVLYREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYREFDEMEEC	1711

> gi|329876|gb|AAA45677.1| polyprotein
Length=2436

Score = 1297 bits (3357), Expect = 0.0, Method: Composition-based stats.
Identities = 683/685 (99%), Positives = 683/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	577	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	636
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	637	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	696
Query	121	dsrgsllsprPISYLKGS SGGPLLC PAGHAVGI FRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKGS SGGPLLC PAGHAVGI FRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	697	DSRGSLLSPRPISYLKGS SGGPLLC PAGHAVGI FRAAVCTRGVAKAVDFIPVENLETTMR	756
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	757	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	816
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	817	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	876
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	877	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	936
Query	361	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIP PIGDVVVVATDALMTGYTG	420

Sbjct	937	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	996
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	997	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1056
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1057	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1116
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1117	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1176
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWV LVGGVLAALAAAYCLSTGCVVIVGRV	660
Sbjct	1177	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWV LVGGVLAALAAAYCLSTGCVVIVGRV	1236
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685 VLSGKPAIIPDREVL YREFDEMEEC	
Sbjct	1237	VLSGKPAIIPDREVL YREFDEMEEC 1261	

> gi|63079188|gb|AA29640.1| polyprotein [Hepatitis C virus]
Length=2889

Score = 1287 bits (3331), Expect = 0.0, Method: Composition-based stats.
Identities = 672/685 (98%), Positives = 681/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQ+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGsllsprPISYLGSSGGPLLCPAGHAVG+ FRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1147	DSRGsllsprPISYLGSSGGPLLCPAGHAVGVFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP PPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLVA+G+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVAMGVNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVREFDEMEEC	685
		VLSGKPAIIPDREVLVREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLVREFDEMEEC	1711

>[gi|55275808|gb|AAV49742.1|](#) polyprotein [Hepatitis C virus]
 Length=2742

Score = 1286 bits (3329), Expect = 0.0, Method: Composition-based stats.
 Identities = 673/685 (98%), Positives = 679/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKGS SGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKGS SGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTI+T TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIDTSTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600




		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVT KYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVT KYIMTCMSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPVT KYIMTCMSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC	685
		VLSGKPAIIPDREVL YREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVL YREFDEMEEC	1711

> [gi|48479030|gb|AAT44836.1|](#) polyprotein [Hepatitis C virus]
 Length=2908

Score = 1286 bits (3328), Expect = 0.0, Method: Composition-based stats.
 Identities = 670/685 (97%), Positives = 680/685 (99%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTN+DQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNIDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKCELA AKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCELA AKLVALGINAVAYYRGLDVSVIPTSGDIVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVT KYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVT KYIMTCMSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVI+GR+	
Sbjct	1627	RLGAVQNEVTLTHPVT KYIMTCMSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIIGRI	1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 VLSGKPA+IPDREVLRYREFDEMEEC
 Sbjct 1687 VLSGKPAVIPDREVLRYREFDEMEEC 1711

>  gi|22129793|ref|NP_671491.1|  polyprotein [Hepatitis C virus]
 gi|2316098|gb|AAB66324.1|  polyprotein [Hepatitis C virus]
 Length=3011

Score = 1286 bits (3328), Expect = 0.0, Method: Composition-based stats.
 Identities = 670/685 (97%), Positives = 678/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLPCPAGHAVG+FRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLPCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		VLSGKPAIIPDREVLRY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLRYQEFDEMEEC 1711	

> gi|6010588|gb|AAF01182.1| polyprotein [synthetic construct]
gi|6010584|gb|AAF01180.1| polyprotein [synthetic construct]
 Length=3015

Score = 1285 bits (3324), Expect = 0.0, Method: Composition-based stats.
 Identities = 669/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1031	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1090
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1091	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1150
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR	
Sbjct	1151	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGTTMR	1210
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1211	SPVFTDNSSPPAVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1270
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1271	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1330
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1331	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1390
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1391	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1450
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1451	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1510
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1511	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1570
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1571	HIDAHFLSQTKQSGENFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1630
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIVGR+	
Sbjct	1631	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAA YCLSTGCVVIVGRI	1690
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1691	VLSGKPAIIPDREVLYQEFDEMEEC	1715

> gi|6010586|gb|AAF01181.1| polyprotein [synthetic construct]
gi|6010582|gb|AAF01179.1| polyprotein [synthetic construct]
 Length=3015

Score = 1285 bits (3324), Expect = 0.0, Method: Composition-based stats.
Identities = 669/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1031	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1090
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1091	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVRRRG	1150
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR	
Sbjct	1151	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGTTMR	1210
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1211	SPVFETDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1270
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1271	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1330
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1331	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1390
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1391	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1450
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1451	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1510
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1511	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1570
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1571	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1630
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1631	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1690
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1691	VLSGKPAIIPDREVLYQEFDEMEEC	1715

>gi|9930557|gb|AAG02099.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 1284 bits (3322), Expect = 0.0, Method: Composition-based stats.
Identities = 669/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVRR+G	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVG+FRFAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFD VIDCNTCVTQTVDLSLDPFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaayYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMTCMSA+ EVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLY+EFDEMEEC	1711

> gi|2327071|gb|AAB67036.1| polyprotein [Hepatitis C virus strain H77]
Length=3011

Score = 1283 bits (3321), Expect = 0.0, Method: Composition-based stats.
Identities = 669/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGT TMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQSGEN PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

>gi|63079190|gb|AA29641.1| polyprotein [Hepatitis C virus]

Length=2885

Score = 1283 bits (3321), Expect = 0.0, Method: Composition-based stats.
Identities = 673/685 (98%), Positives = 678/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQARS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMS+AHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGEN PVLVAQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLRYREFDEMEEC	1711

> [gi|55275810|gb|AAV49743.1|](#) polyprotein [Hepatitis C virus]
Length=2742

Score = 1282 bits (3318), Expect = 0.0, Method: Composition-based stats.
Identities = 670/685 (97%), Positives = 676/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALSTTGEIPFYGKAIPLE IK LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLV LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVVLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTI+ TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTIDISTLTPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV RLGAVQNE+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 VLSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLRYREFDEMEEC 1711	

> [gi|63079194|gb|AA29643.1|](#) polyprotein [Hepatitis C virus]

Length=2883

Score = 1281 bits (3315), Expect = 0.0, Method: Composition-based stats.
Identities = 669/685 (97%), Positives = 678/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSV	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446

Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQ E+TLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQTEVTLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAIIPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYREFDEMEEC	1711

> [gi|2327075|gb|AAB67038.1|](#) polyprotein [Hepatitis C virus strain H77]
Length=3011

Score = 1280 bits (3312), Expect = 0.0, Method: Composition-based stats.
Identities = 667/685 (97%), Positives = 675/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY QQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYTQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS L PCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LAPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGT TMR	1206
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTQSGEN PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQSGENFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|9843677|emb|CAC03609.1| unnamed protein product [Hepatitis C virus]
Length=3011

Score = 1278 bits (3308), Expect = 0.0, Method: Composition-based stats.
Identities = 666/685 (97%), Positives = 677/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D RGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAV+F+PVENLETTMR	180
Sbjct	1147	DGRGSLLSPRPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVEFVPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNS+PP VPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSAPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHSNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCD+LAAKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDDLAAKLVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDS+VLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSAVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHG TPLLY	600
Sbjct	1567	HIDAHFLSQTQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGSTPLLY	1626

Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTKYIMTCMSADLE+VTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMTCMSADLEIVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686

Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKP IIPD+EVLYREFDEMEEC	
Sbjct	1687	VLSGKPPIIPDQEVLYREFDEMEEC	1711

> gi|221587|dbj|BAA01582.1| polyprotein precursor [Hepatitis C virus]
 Length=3011

Score = 1278 bits (3308), Expect = 0.0, Method: Composition-based stats.
 Identities = 665/685 (97%), Positives = 674/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLKSSGGPLLCPAGH VGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DSRGSLSPRPISYLKSSGGPLLCPAGHVVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206

Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATS+	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSV	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPH NIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHANIEEVALSTTGEIPFYGKAIPLEAIK	1386

Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLVALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446

Query	421	DFDSVIDCNTCVTQTVDfSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDfSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDfSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSS+LCECYD GCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSILCECYDTGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ GEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQGGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626

Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQ E+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQGEVTLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686

Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
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VLSG+PAIIPDREVLRYREFDEMEEC
 Sbjct 1687 VLSGRPAIIPDREVLRYREFDEMEEC 1711

> gi|63079186|gb|AA29639.1| polyprotein [Hepatitis C virus]
 Length=2889

Score = 1278 bits (3308), Expect = 0.0, Method: Composition-based stats.
 Identities = 669/685 (97%), Positives = 676/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFETDSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFETDSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQ ETAGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQXETAGARLVVLATATPPGSVTVPHXNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKLV LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKVTLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCN CVTQTVDVDFSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNICVTQTVDVDFSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLRYREFDEMEEC 1711	

> gi|2327073|gb|AAB67037.1| polyprotein [Hepatitis C virus strain H77]
 Length=3011

Score = 1278 bits (3308), Expect = 0.0, Method: Composition-based stats.
Identities = 667/685 (97%), Positives = 675/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLT RDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLT SRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVG+FRAAVCTRGVAKAVDFIPVENL TTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGLFRAAVCTRGVAKAVDFIPVENLGTTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDN SPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNPSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

> [gi|63079196|gb|AAI29644.1|](#) polyprotein [Hepatitis C virus]
Length=2889

Score = 1275 bits (3300), Expect = 0.0, Method: Composition-based stats.
Identities = 668/685 (97%), Positives = 676/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIV TAAQTFLATCINGVCWTVYHGAG	

Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVXTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMTNV+QDL+GWPAPQG+RSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS TVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	LSGKPAIIPDREVLYREFDEMEEC	1711

> [gi|130461|sp|P27958|POLG_HCVH](#) Genome polyprotein [Contains: Core protein p21 (Capsid) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|329738|gb|AAA45534.1|](#) polyprotein
 Length=3011

Score = 1268 bits (3281), Expect = 0.0, Method: Composition-based stats.
 Identities = 663/685 (96%), Positives = 672/685 (98%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60

Sbjct	1027	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQ YTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQTYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLLCP GHAVG+FRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPTGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAA+GYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAKGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTGSPITYSTY GKFLAD GCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGSPITYSTY GKFLADAGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK GIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	SGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPTSGDVVVVSTDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHL FWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLGFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQM KCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMRKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaayCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|63079184|gb|AA29638.1| polyprotein [Hepatitis C virus]
Length=2882

Score = 1263 bits (3268), Expect = 0.0, Method: Composition-based stats.
Identities = 661/685 (96%), Positives = 674/685 (98%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIA+PKGPVIQMYTNVDQDLVGWPAPQG+RSLTPC CGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIATPKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCACGSSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKCHGVDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIPLE+IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSK+KC++LAALKLVA G+NAVAYYRGLDVSVIP G+VVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	+FDSVIDCNTCVTQTVDFSLDPTF IET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlalaayCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTKYIMTMSADLEVVTSTWVVLVGGVLAALAAAYCLSTGCVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSGKPAIIPDREVLYREFDEMEEC	1711

> gi|7650260|gb|AAE65961.1| polyprotein [Hepatitis C virus]

Length=3010

Score = 1234 bits (3193), Expect = 0.0, Method: Composition-based stats.
Identities = 636/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTYVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP GSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240

Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTG RTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	300
Sbjct	1267	YMSKAHGIDPNIRTGARTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQEFDEMEEC 1711	

>gi|11559457|dbj|BAB18808.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1234 bits (3193), Expect = 0.0, Method: Composition-based stats.
Identities = 635/685 (92%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA KLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELATKLVALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlgvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQN++TLTHPVTK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNDVTLTHPVTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQEFDEMEEC 1711	

>gi|7650232|gb|AAF65947.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1233 bits (3190), Expect = 0.0, Method: Composition-based stats.
Identities = 633/685 (92%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVVSTATQSF LATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGP LCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGP LCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPT GSGKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPT GSGKST+VPAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVF TDNSSPPAVPQTFQVAHLHAPT GSGKSTRVPAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTIT TGGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTG+RTIT TGG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGIRTIT TGGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPSIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420

Sbjct	1387	GGRHLIFCHSKKKKCELAACL ALGINAV+YYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAACLALGINAVSYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDLSLPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLPTFTTITETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVlvvggvlaalaaYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKFIMACMSADLEVVTSTWVlvvggvlaalaaYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSG+PAIIPDRE LY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREALYQEFDEMEEC 1711	

> [gi|5918947|gb|AAD56189.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1233 bits (3189), Expect = 0.0, Method: Composition-based stats.
Identities = 634/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPVTQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLGSSGGPLLCP GH VG+FAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKGSSGGPLLCPLGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE+IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEIIK	1386
Query	361	GGRHLIFCHSKKKKCELAACLALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAACL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAACLALGVNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDLSLPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLPTFTTITETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	TLSGRPAIIPDREVLYQEFDEMEEC 1711	

>gi|5918965|gb|AAD56198.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1232 bits (3188), Expect = 0.0, Method: Composition-based stats.
Identities = 634/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPFGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCP GH VGIFRAAVCTRGVAKAVDFIPVE++ET+MR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPGLGHVVGIFRAAVCTRGVAKAVDFIPVESMETSMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE ALS TGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEAALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA+KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAASKLSALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMGIRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600

Sbjct	1567	HIDAHFLSQTQK+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP LHGPTPLLY HIDAHFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPVLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TK+IMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKFIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSG+PAIIPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLRYREFDEMEEC 1711	

> [gi|130458|sp|P26663|POLG_HCVBK](#) Genome polyprotein [Contains: Core protein p21 (Cap: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|329771|gb|AAA72945.1|](#) [Hepatitis C virus core, matrix, envelope and non-structural protein RNA.], gene product
 Length=3010

Score = 1232 bits (3188), Expect = 0.0, Method: Composition-based stats.
 Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A+PKGP+ QMYTNVDQDLVGWP P G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAAPKGPITQMYTNVDQDLVGWPKPPGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLC PAGHVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLGSSGGPLLC P GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLGSSGGPLLC PFGHVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTG+P+TYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGAPVITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I+	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIR	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP IGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA AKL LGINAVAYYRGLDVSVIP IGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSGLGINAVAYYRGLDVSVIPTIGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtgrgrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPPLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		+LSG+PAI+PDRE+LY+EFDEMEEC	
Sbjct	1687	ILSGRPAIVPDRELLYQEFDEMEEC	1711

>gi|12831193|gb|AAK08509.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1232 bits (3187), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPOGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFSQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFSQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFSQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTG+P+TYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGAPVTYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I+	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIR	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK LGINAVAYYRGLDVSVIP IGDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKSGLGINAVAYYRGLDVSVIPITIGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTTETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660

Sbjct 1627 RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSG+PAI+PDRE+LY+EFDEMEEC
 Sbjct 1687 ILSGRPAIVPDRELLYQEFDEMEEC 1711

>gi|7650246|gb|AAF65954.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1232 bits (3187), Expect = 0.0, Method: Composition-based stats.
 Identities = 635/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG
 Sbjct 1027 APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 ++T+A PKGPVIQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1087 SKTLAGPKGPVIQMYTNVDQDLVGWPAPPGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR
 Sbjct 1147 DSRGSLSPRPISYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKA+G+DPNIRTGVRTITTTG+ ITYSTYGKFLADGGCSGGAYDII+CDECHSTD+TSI
 Sbjct 1267 YMSKAYGVDPNIRTGVRTITTTGASITYSTYGKFLADGGCSGGAYDIIMCDECHSTDSTSI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKCELAALK ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG
 Sbjct 1387 GGRHLIFCHSKKKKCELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG 1446

Query 421 DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWD MWKCL RLKPTLHGPTPLLY
 Sbjct 1567 HIDAFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDLMWKCLTRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSGKPAIIPDREVLRYREFDEMEEC
 Sbjct 1687 ILSGKPAIIPDREVLRYREFDEMEEC 1711

> gi|5918945|gb|AAD56188.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1232 bits (3187), Expect = 0.0, Method: Composition-based stats.
Identities = 634/685 (92%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGPV QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPVTQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP GHAVG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPLGHAVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE+IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEIIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALK ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	TLSGRPAIIPDREVLYQEFDEMEEC	1711

> gi|7650244|gb|AAF65953.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1231 bits (3186), Expect = 0.0, Method: Composition-based stats.

Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRP+SYLKSSGGPLLCP GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G DPNIRTG+RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIP+EVIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	+FDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPA+IPDREVLYREFDEMEEC 1711	

> [gi|5918939|gb|AAD56185.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1231 bits (3186), Expect = 0.0, Method: Composition-based stats.
 Identities = 629/685 (91%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A P+GP+ QMYTNVDQDLVGW AP GSRSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPQGPITQMYTNVDQDLVGWQAPPGSRSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFEQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SP+FTDNSSPP VPQ+EQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1207	SPIFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+ VIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIGVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		+LSG+PA+IPDRE+LYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREILRYREFDEMEEC	1711

> gi|5918937|gb|AAD56184.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1231 bits (3186), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A P+GP+ QMYTNVDQDLVGW AP GSRSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPQGPITQMYTNVDQDLVGWQAPPGSRSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	

Sbjct	1147	DTRGSLSPRPVSYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SP+FTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	SPIFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDII+CDECHSTD+TSI	360
Sbjct	1327	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIMCDECHSTDSTSI	1386
Query	361	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	420
Sbjct	1387	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIGVIK	1446
Query	421	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	480
Sbjct	1447	GGRHLIFCHSKKKKDELA AKL ALG+NAVAYYRGLDVSVIP GDV VVVATDALMTG+TG	1506
Query	481	GGRHLIFCHSKKKKDELA AKLSALGLNAVAYYRGLDVSVIPTSGDV VVVATDALMTGFTG	540
Sbjct	1507	DFDSVIDCNCVTVQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	1566
Query	541	DFDSVIDCNCVTVQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	600
Sbjct	1567	DFDSVIDCNCVTVQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1626
Query	601	RPSGMFDSSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	660
Sbjct	1627	RPSGMFDSSSVLCECYDAGCAWYELTPAETT VRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	1686
Query	661	RPSGMFDSSSVLCECYDAGCAWYELTPAETT VRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	685
Sbjct	1687	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1711
Query	601	HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1627	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	ILSGRPAVIPDREILYREFDEMEEC	685
Sbjct	1687	+LSG+PA+IPDRE+LYREFDEMEEC	1711

>gi|46560636|gb|AAT00644.1| polyprotein [Hepatitis C virus]
Length=3014

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1031	APITAY+QQTRGLLGCI+TSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1090
Query	61	APITAYSQQTRGLLGCIIVTSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	120
Sbjct	1091	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYL VTRHADVIPVrrrg	1150
Query	121	++T+A PKGP+IQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYL VTRHADVIPVRRRG	180
Sbjct	1151	SKTLAGPKGPPIQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYL VTRHADVIPVRRRG	1210
Query	181	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	240
Sbjct	1211	DSRGSLLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1270
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1211	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1270

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1271	YMSKAYGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1330
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHP+IEEVALS GEIPFYGKAIP+EVIK	
Sbjct	1331	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPSIEEVALSNIGEIPFYGKAIPLEVIK	1390
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1391	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1450
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1451	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTMPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1510
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1511	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1570
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYL+AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1571	HIDAHFLSQTKQAGENFPYLIAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1630
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1631	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1690
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		VLSGKPAIIPDRE LY+EFDEMEEC	
Sbjct	1691	VLSGKPAIIPDREALYQEFDEMEEC 1715	

> [gi|23957857|gb|AAD44718.2|](#) polyprotein [Hepatitis C virus]
 Length=3015

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
 Identities = 628/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1028	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1088	SKTLAGPKGPVIAQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKGS SGGPLLCP+GHAVG+FRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1148	DNRGSLLSPRPVSYLKGS SGGPLLCPSGHAVGVFRAAVCTRGVAKAVDFVPVESMETTMR	1207
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKST+VPAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1208	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTRVPAAYAAQGYKVLVNLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+T+I	
Sbjct	1268	YMSKAHGTDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTTI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	

Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1387
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1388	GGRHLIFCHSKKKCDELAALKLSGLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1447
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1628	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1688	ILSGRPAVVPDREVLYREFDEMEEC 1712	

> [gi|7650266|gb|AAF65964.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG+RTITTTG+PITYSTYGKFLADGGCSGGAYDII+CDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGIRTITTTGAPITYSTYGKFLADGGCSGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSNLGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

>gi|5821155|dbj|BAA83719.1| polyprotein [Hepatitis C virus]
Length=3013

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
Identities = 635/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLG IITSLTGRDKN+VEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1028	APITAYSQQTRGLLGSIITSLTGRDKNRVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPTCTGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLT CTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1088	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSLTSCCTGSSDLYLVTRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1148	DSRGSLSPRPVSYLKSSGGPLLCPSGHTVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1207
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1208	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1268	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1387
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL ALGINAVAYYRGLDVSVIP GD VVVATDALMTGYTG	
Sbjct	1388	GGRHLIFCHSKKKCDELA AKLSALGINAVAYYRGLDVSVIPTSGDAVVVATDALMTGYTG	1447
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSV DCNTCVTQTVDFSLDPTFTTET T+PQD+VSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVTD CNTCVTQTVDFSLDPTFTTETTTVPQDSVSRSQRRGRTGRGRGGIYRFVIPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	


Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1628	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685	
		+LSG+PAIIPDREVLVREFDEMEEC	
Sbjct	1688	ILSGRPAIIPDREVLVREFDEMEEC 1712	

> gi|87080431|emb|CAH64686.1| polyprotein [Hepatitis C virus]
 Length=3011

Score = 1231 bits (3184), Expect = 0.0, Method: Composition-based stats.
 Identities = 633/685 (92%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVST +QTFLATC+NGVCWTVYHGAG	
Sbjct	1028	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTTSQTFLATCVNGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+++A PKGP++QMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1088	AKSLAGPKGPILQMYTNVDQDLVGWPAPQGTSLTPCTCGSSDLYLVTRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF+PVE++ET MR	
Sbjct	1148	DTRGSLLSPRPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFVPVESMETVMR	1207
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SP FTDNS+PP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1208	SPTFTDNSTPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1268	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAET GAR+VVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIPLEVIK	
Sbjct	1328	LGIGTVLDQAETCGARMVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPLEVIK	1387
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL +LG+NAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	1388	GGRHLIFCHSKKKCDELA AKLTSGLNAVAYYRGLDVSVIPLSGDV VVVSTDALMTGFTG	1447
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCN CVTQTVD FSLDPTFTIET TLPQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVIDCNVCVTQTVD FSLDPTFTIETTTLPQDAVSRSQRRGRTGRGRLGIYRFVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAYMNTPLPVCQDHLEFWE VFTGLT	
Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYMNTPLPVCQDHLEFWESVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARA APPPSWDQMWKCLIRLKPTL GPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVAIQATVCARASAPPPSWDQMWKCLIRLKPTLRGPTPLLY	1627

Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGG+LAALAAAYCLSTG VVIVGR+	
Sbjct	1628	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGILAAALAAAYCLSTGSVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1688	VLSGKPAIIPDREVLYKEFDEMEEC	1712

>  gi|5918967|gb|AAD56199.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1230 bits (3183), Expect = 0.0, Method: Composition-based stats.
Identities = 633/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPTCTGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCP GH VGIFRAAVCTRGVAKAVDFIPVE++ET+MR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCP LGHVVGIFRAAVCTRGVAKAVDFIPVESMETSMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE ALS TGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA+KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAASKLSALGVNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQ KQ+G+N PYLVAIQATVCARAQAPPPSWDMWKCLIRLKP LHGPTPLLY	
Sbjct	1567	HIDAHFLSQNKQAGDNFPYLVAIQATVCARAQAPPPSWDMWKCLIRLKPVLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK+IMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITK FIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PAIIPDREVLYREFDEMEEC	

Sbjct 1687 ILSGRPAPIPDREVLYREFDEMEEC 1711

> gi|11559469|dbj|BAB18814.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1230 bits (3183), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCI+TSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIIVTSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLSLPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLGSSGGPLLCPSGHIVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ++QVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTYQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+ ITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGASITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL +LGINAVAYYRGLDVSVIP G+VVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSSLGINAVAYYRGLDVSVIPASGNVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

> gi|48237634|gb|AAT40682.1| polyprotein [Hepatitis C virus]
Length=3013

Score = 1230 bits (3182), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVS+IP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGVNAVAYYRGLDVSIIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARA+APPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAKAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> [gi|1212742|dbj|BAA08120.1|](#) HCV polyprotein [Hepatitis C virus]
Length=3010

Score = 1230 bits (3182), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCP+GH VGI FRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFTDNS+PP VPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AAKL ALG+NAVAYYRGLDVS+IP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKLSALGVNAVAYYRGLDVSIIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL VAYQATVCARA+APPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAKAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITK FIMACSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> gi|7650248|gb|AAF65955.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCING CWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGACWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+IQMYTNVD DLVGW P G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGP I IQMYTNVDLDLVGWQVPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	DSRGSLLSPRP+SYLKSSGGPLLCP GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR DSRGSLLSPRPVSYLKSSGGPLLCP LGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPV+TDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVYTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVR ITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIDPNIRTGVRITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCAR+QAPPPSWDQMWKCL+RLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARSQAPPPSWDQMWKCLLRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlgvgvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> gi|7650236|gb|AAF65949.1| polyprotein [Hepatitis C virus]
Length=3013

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 667/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCINGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPV RRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVHRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T++	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGE+PFYGKAIP+EVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLC+CYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+GEN PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTK+IM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSG+PA+IPDREVLYREFDEMEEC 1711	

> [gi|5918951|gb|AAD56191.1](#) polyprotein [Hepatitis C virus]
Length=3013

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1030	APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1089
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1090	+T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADV+PVRRRG	1149
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1150	DSRGSLSPRP+SYLKSSGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR	1209
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1210	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1269
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1270	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	1329
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1330	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVI+ LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP+EVIR	1389
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA KL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1390	GGRHLIFCHSKKKKCELATKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1449
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1450	DFDSVIDCNCVTQTQTVDFSLDPTFTTIETTTVPQDAVSR+QRRGRTGRGRGGIYRFVTPGE	1509
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1510	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1569
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1570	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1629
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1630	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1689
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSG+PA+IPDREVLRY+EFDEMEEC	
Sbjct	1690	ILSGRPAVIPDREVLRYQEFDEMEEC 1714	

> [gi|266820|sp|Q00269|POLG_HCVJT](#) Genome polyprotein [Contains: Core protein p21 (Cap: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|221613|dbj|BAA01943.1|](#) polyprotein [Hepatitis C virus]
[gi|384057|prf|1904413A](#) polyprotein
 Length=3010

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
 Identities = 631/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWHAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D RGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGTDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LGINAVAYYRGLDVSVIP GDVV+VATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSGLGINAVAYYRGLDVSVIPTSGDVVIVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlgvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		+LSG+PA++PDREVLRYREFDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLRYREFDEMEEC	1711

> [gi|464178|dbj|BAA03581.1](#) polyprotein [Hepatitis C virus (isolate HC-G9)]
[gi|81992806|sp|Q81754|POLG_HCVH9](#) Genome polyprotein [Contains: Core protein p21 (Caps C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
 Length=3011

Score = 1229 bits (3181), Expect = 0.0, Method: Composition-based stats.
 Identities = 635/685 (92%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTA QTFLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+RTIAS GPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCG+SDLYLVTRHADVIPVRRRG	
Sbjct	1087	SRTIASASGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGASDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLGSSGGPLLC P GHAVGIFRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1147	DNRGSLLSPRPISYLGSSGGPLLC PMGHAVGIFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPTVPQSYQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTGSPIT+STYGKFLADGGCSGGAYDIIICDECHS DATSI	

Sbjct	1267	YMSKAHGIDPNVRTGVRTITTTGSPITHSTYKFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RL +LATATPPGSVTVPH NIEEVALST GEIPFYGKAIPL IK	
Sbjct	1327	LGIGTVLDQAETAGVRLTILATATPPGSVTVPHSNIEEVALSTEGEIPFYGKAIPLNYIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKV LG+NAVA+YRGLDVSVIP GDV VVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKVLGLVNAVAFYRGLDVSVIPPTGDV VVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCV QTVD FSLDPTF+IET T+PQDAVSR+QRRGRTGRGK GIYR+V+PGE	
Sbjct	1447	DFDSVIDCNTCVVQTVD FSLDPTFSIETSTVPQDAVSRSQRRGRTGRGKHGIYRYVSPGE	1506
Query	481	RPSGMFDSVVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDS VLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSVVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVA YQATVCARA+APPPSWDQMWKCLIRLKPTL G TPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVA YQATVCARAKAPPPSWDQMWKCLIRLKPTLTGATPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLG VQNEITLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLSTG VVIVGR+	
Sbjct	1627	RLGGVQNEITLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSGKPA+IPDREVL YREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVL YREFDEMEEC 1711	

> gi|11559447|dbj|BAB18803.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1229 bits (3180), Expect = 0.0, Method: Composition-based stats.
 Identities = 633/685 (92%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQT RGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQT RGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQT RGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAH+HAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHIHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALS TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSNTGEIPFYGKAIPLEAIK	1386

Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKLSGLGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ G YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGTYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGM DSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMLDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|5918949|gb|AAD56190.1| polyprotein [Hepatitis C virus]

Length=3013

Score = 1229 bits (3179), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1030	APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1089
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADV+PVRRRG	
Sbjct	1090	AKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVVPVRRRG	1149
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1150	DSRGSLSPRPVS YLGSSGGPLLCPSGHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR	1209
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1210	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	1269
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1270	YMSKAHGVDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTSI	1329
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVI+	
Sbjct	1330	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIR	1389
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA KL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1390	GGRHLIFCHSKKKKCELA TKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1449
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	

Sbjct	1450	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1509
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1510	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1569
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1570	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1629
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVlvvggvlaalaaYCL+TG VVIVGR+	660
Sbjct	1630	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVlvvggvlaalaaYCLTTGSSVVIVGRI	1689
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1690	ILSGRPAIIPDREVLYQEFDEMEEC 1714	

> gi|5441839|emb|CAB46915.1| non-structural polyprotein [Hepatitis C virus]
gi|5441833|emb|CAB46911.1| non-structural polyprotein [Hepatitis C virus]
Length=2201

Score = 1229 bits (3179), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	218	APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	277
Query	61	TRTIASPKGPVIMYTNVDQDLVGWPAPOGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	278	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	337
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	338	DSRGSLLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	397
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	398	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	457
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	458	YMSKAHGIDPNIRTGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	517
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS+TGEIPFYGKAIP+E IK	360
Sbjct	518	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSSTTGEIPFYGKAIPETIK	577
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVATDALMTGYTG GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	420
Sbjct	578	GGRHLIFCHSKKKCDELA AKLSGLGLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG	637
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	638	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	697
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	698	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	757

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Query   541  HIDAHFSLQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600
          HIDAHFSLQTKQ+G+N PYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   758  HIDAHFSLQTKQAGDNFPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  817

Query   601  RLGAVQNEITLTHPVTKYIMTCMSADLEVVVTSTWvlggvlalaaYCLSTGCVVIVGRV  660
          RLGAVQNE+T THP+TKYIM CMSADLEVVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
Sbjct   818  RLGAVQNEVTTHPITKYIMACMSADLEVVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI  877

Query   661  VLSGKPAIIPDREVLVREFDEMEEC  685
          +LSGKPAIIPDREVLVREFDEMEEC
Sbjct   878  ILSGKPAIIPDREVLVREFDEMEEC  902

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>gi|5420377|emb|CAB46677.1| polyprotein [Hepatitis C virus type 1b]
 gi|68565847|sp|Q9WMX2|POLG HCVCO Genome polyprotein [Contains: Core protein p21 (Caps C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
 Length=3010

Score = 1228 bits (3178), Expect = 0.0, Method: Composition-based stats.
 Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

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Query    1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG  60
          APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
Sbjct   1027  APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG  1086

Query    61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg  120
          ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct   1087  SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG  1146

Query   121  dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR  180
          DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
Sbjct   1147  DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR  1206

Query   181  SPVFETDNSSPPVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA  240
          SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct   1207  SPVFETDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA  1266

Query   241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI  300
          YMSKAHGIDPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I
Sbjct   1267  YMSKAHGIDPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI  1326

Query   301  LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK  360
          LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS+TGEIPFYGKAIP+E IK
Sbjct   1327  LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSSTGEIPFYGKAIPETIK  1386

Query   361  GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG  420
          GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG
Sbjct   1387  GGRHLIFCHSKKKKCELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG  1446

Query   421  DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE  480
          DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
Sbjct   1447  DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE  1506

Query   481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT  540
          RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPPLPVCQDHLEFWE VFTGLT

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Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+T THP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTTTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAIIPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYREFDEMEEC 1711	

> gi|62006147|dbj|BAD91386.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
 Identities = 630/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGFVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DNRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKA P+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAFFIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA KL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELATKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSGKPA+IPDREVLY+EFDEMEEC
 Sbjct 1687 ILSGKPAVIPDREVLYQEFDEMEEC 1711

> gi|5738247|gb|AAD50312.1| polyprotein precursor [Hepatitis C virus]
 Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
 Identities = 631/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
 Sbjct 1027 APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 T+T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1087 TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
 Sbjct 1147 DSRGSLSPRPISYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQS FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG+DPN+RTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAHGVDPNLRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E+IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPIEIK 1386

Query 361 GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKDELAALK LG+NAVAYYRGLDVSVIP G+VVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSKKKKDELAALKSLGLLNAVAYYRGLDVSVIP TSGNVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NT PGLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNT PGLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNETTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 VLSGKPAIIPDREVLY+EFDEMEEC

Sbjct 1687 VLSGKPAIIPDREVLVYQEFDEMEEC 1711

> gi|7650228|gb|AAF65945.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPPIAQMVTNVDQDLVGWAAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+ IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPATIK	1386
Query	361	GGRHLIFCHSKKKKDELAACLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAACL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAACLALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPODAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+URLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVURLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVYREFDEMEEC 685	
		+LSG+PA+IPDREVLVY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLVYQEFDEMEEC 1711	

> gi|5918957|gb|AAD56194.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPPLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPPLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTG+RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGTDPNIRTGIRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSALGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWEVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

>gi|5918929|gb|AAD56180.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3177), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG SKTLAGPKGPPIAQMNTNVDQDLVGWAAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+ IK LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIP IATIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVTLTHPVTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSG+PA+IPDREVLY+EFDEMEEC ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> gi|7650256|gb|AAF65959.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3176), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGL GCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG APITAYAQQTRGLFGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRR SKTLAGPKGPITQMYTNVDQDLVGWQAPSGARSLTPCTCGSSDLYLVTRHADVIPVRRRS	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	D RGSLLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR DGRGSLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPV+TDNSSPP VPQSFQVAHLHAPTGSGBKST+VPAAYAAQGYKVLVLNPSVAATLGFG	240
Sbjct	1207	SPVYTDNSSPPAVPQSFQVAHLHAPTGSBKSTRVPAAYAAQGYKVLVLNPSVAATLGFGT	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAAL+L ALGINAVAYYRGLDVS+IP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALQTLALGINAVAYYRGLDVSIIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQD+VSR+QRRGRTGRG+ GIYR+V PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDSVSRSQRRGRTGRGRGGIYRYVIPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TKYIM CMSADLE+VTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKYIMACMSADLEIVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYREFDEMEEC 1711	

> gi|7650222|gb|AAF65942.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1228 bits (3176), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+RGSLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DTRGSLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+++IK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
Sbjct	1687	+LSG+PA++PDREVLRY+FDEMEEC 1711	

>gi|46560634|gb|AAT00643.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1227 bits (3175), Expect = 0.0, Method: Composition-based stats.
Identities = 633/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEI FYGKAIP+EVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNAGEISFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSGKPA+IPDREVLRY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLRYQEFDEMEEC 1711	

> gi|11559455|dbj|BAB18807.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 1227 bits (3175), Expect = 0.0, Method: Composition-based stats.
Identities = 633/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1028	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1088	SKTLAGPKGPVTQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLKSSSGGPLLCP GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1148	DSRGSLSPRPVSYLKSSSGGPLLCPPLGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1207
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1208	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTVGRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+GIDPN+RTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	300
Sbjct	1268	YMSKAYGIDPNVRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK	360
Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK	1387
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA KL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1388	GGRHLIFCHSKKKCDELATKLSGLGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1447

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1628	RLGAVQNEITLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTG SVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1688	ILSGRPAIIPDREVLYQEFDEMEEC 1712	

> [gi|7650240|gb|AAF65951.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1227 bits (3174), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++ +A KGPV QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKALAGQKGPVTQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVF TDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYA+QGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVF TDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYASQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQK+G+N PYL AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQAGDNFPYLTAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TGCVVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA+IPDR+VLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDRDVLYQEFDEMEEC 1711	

> gi|11559451|dbj|BAB18805.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1227 bits (3174), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLKGSSGGPLLCP GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLKGSSGGPLLCPLGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA KL ALGINAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELATKLSALGINAVAYYRGLDVSVIPTSGNVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTMPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQK+GENLPYLVAYQATVCARAQAPPPSWDQMWKCL+RLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTQKAGENLPYLVAYQATVCARAQAPPPSWDQMWKCLVRLKPTLQGPTPLLY	1626

Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		VLSG+PA++PDREVLY+EFDEMEEC	
Sbjct	1687	VLSGRPAVVPDREVLYQEFDEMEEC	1711

> gi|11559445|dbj|BAB18802.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1227 bits (3174), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAV+FIPVE++ETTMR	
Sbjct	1147	DNRGSLLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVEFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALK+ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLLALGVNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVFDLPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVFDLPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVFDLPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G++ PYLVAQATVCARAQAPPPSWDMWKCL RLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDHFPYLVAQATVCARAQAPPPSWDMWKCLTRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IMTCM+ADLE+ TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMTCMAADLEIATSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685

+LSG+PA++PDREVLY+EFDEMEEC
 Sbjct 1687 ILSGRPAVVPDREVLYQEFDEMEEC 1711

> gi|471117|dbj|BAA01728.1| polyprotein precursor [Hepatitis C virus]
 Length=3010

Score = 1227 bits (3174), Expect = 0.0, Method: Composition-based stats.
 Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVR+ADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSRLTPCTCGSSDLYLVRTRYADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKGSSGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKGSSGGPLLCPSGHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTQFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN RTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHSNIEEVALSTTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		VLSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	VLSGRPAVIPDREVLYQEFDEMEEC 1711	

> gi|5918953|gb|AAD56192.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1226 bits (3173), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg	120
		++T+A P+GP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLVLRHADVIPVRRRG	
Sbjct	1087	SKTLAGPQGPITQMYTNVDQDLVGWPAPSGARSLTPCTCGSSDLVLRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SP+FTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPIFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		Y+SKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YVSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAGKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET+T+PQDAVSR+QRRGRTGRG+ G YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETMTVPQDAVSRSQRRGRTGRGRRGTYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTK IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKLIMCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPVAVVPDREVLYREFDEMEEC 1711	

>gi|11559449|dbj|BAB18804.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3173), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	

Sbjct	1027	APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKGS SGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE +ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKGS SGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVEAMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG DPNIRTG+RTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGTDPNIRTGIRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA AAKL +LGINAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKLSSLGINAVAYYRGLDVSVIP TSGNVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRTQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> [gi|2764398|emb|CAA03854.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3172), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG APITAYSQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPVTQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VP++FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPETFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPLETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKSGLGLNAVAYYRGLDVSVIPTSGDIVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+URLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSURLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYL AYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLTAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVVLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685	
		+LSG+PAIIPDREVLV+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLVQEFDEMEEC 1711	

> gi|56342187|dbj|BAD73971.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1226 bits (3172), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	

Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPG SVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPG SVTVPHPNIEEVALSNVGEIPFYGKAIP IETIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCELA AAKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAIIPDREVLY++FDEMEEC 1711	

>gi|7341103|gb|AAF61205.1| polyprotein [Hepatitis C virus]
Length=3008

Score = 1226 bits (3172), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1025	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	1084
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1085	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1144
Query	121	dsrgsllsprPISYLGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1145	DSRGSLSPRP+SYLGSSGGP LLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1204
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1205	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1264
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1265	YMSKAHG+DPNIRTG RT+TTG+PITYSTY GKFLADGGCSGGAYDII+CDECHSTD+TSI	1324

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1325	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1384
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA KL LGINAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1385	GGRHLIFCHSKKKCDELATKLSGLGINAVAYYRGLDVSVIPASGNVVVVATDALMTGYTG	1444
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1445	DFDSVIDCNCVTQTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1504
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1505	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1564
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1565	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1624
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1625	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1684
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1685	ILSGKPAVIPDREVLYREFDEMEEC 1709	

> gi|7650234|gb|AAF65948.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVG+FAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGLFAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	

Sbjct	1387	GGRHLIFCHSKKKKCELAALKLTGLGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTI+T T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIDTTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYQEFDEMEEC 1711	

> gi|5918955|gb|AAD56193.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A P+GP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPQGPITQMYTNVDQDLVGWPAPSGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLSPRP+SYLKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SP+FTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPIFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		Y+SKAHGIDPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	
Sbjct	1267	YVSKAHGIDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAGKLSALGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET+T+PQDAVSR+QRRGRTGRG+ G YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETMTVPQDAVSRSQRRGRTGRGRRGTYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLTRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTK IM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPVTKLIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLYREFDEMEEC 1711	

> [gi|5918931|gb|AAD56181.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPPIAQMYTNVDQDLVGWAAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+ IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIP IATIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTRGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	

Sbjct 1567 HIDAFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHPVTK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+

Sbjct 1627 RLGAVQNEVTLTHPVTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSG+PA+IPDREVLY+EFDEMEEC

Sbjct 1687 ILSGRPAVIPDREVLYQEFDEMEEC 1711

> gi|266821|sp|P29846|POLG_HCVTW Genome polyprotein [Contains: Core protein p21 (Cap: C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
 Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG

Sbjct 1027 APITAYAQQTRGLFGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVDQDLVGW APQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG

Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGWHAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR

Sbjct 1147 DSRGSLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA

Sbjct 1207 SPVFTDNSSPPAVPQAFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+T+I

Sbjct 1267 YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK

Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKCDELA AKL ALGI+AVAYYRGLDVSVIP G+VVVVATDALMTG+TG

Sbjct 1387 GGRHLIFCHSKKKCDELA AKLSALGIHAVAYYRGLDVSVIPASGNVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRT RG+ GIYRFV PGE

Sbjct 1447 DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTMPQDAVSRSQRRGRTSRGRRGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT

Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
 HIDAFLSQTQK+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY

Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

> gi|11559441|dbj|BAB18800.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1226 bits (3171), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+QFVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLV+LATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVLLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLSALGVNAVAYYRGLDVSVIPTSGNVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDfSLDPTFTIETITLTPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDfSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDfSLDPTFTIETTTVPQDAVSRQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTRLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTRLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTRLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686

Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSGKPA+IPDREVLVREFDEMEEC
 Sbjct 1687 ILSGKPAVIPDREVLVREFDEMEEC 1711

> gi|56342185|dbj|BAD73970.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
 Identities = 629/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
 Sbjct 1027 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg 120
 T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLVLRHADVIPVRRRG
 Sbjct 1087 TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLVLRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
 Sbjct 1147 DSRGSLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNVGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHS+KKCDELAACKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSRKKCDELAACKLSSLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVDFSLDPTFTTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTVPQDAVSRQRRGRTGRGRTGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY
 Sbjct 1567 HIDAFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMCMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVIVGRI 1686

Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSGKPAIIPDREVLV++FDEMEEC
 Sbjct 1687 ILSGKPAIIPDREVLVQQFDEMEEC 1711

> gi|7650254|gb|AAF65958.1| polyprotein [Hepatitis C virus]

Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGL+GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYTGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYTGKFLADGGCSGGAYDII+CDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL ALGINAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAQATVCARAQA PPSWDQMWKCL RLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPA+IPDREVLYREFDEMEEC 1711	

>gi|5918933|gb|AAD56182.1| polyprotein [Hepatitis C virus]

Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
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Sbjct	1027	APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPN+RTGVRTITTTG+ ITYSTYKFLADGGCSGGAYDII+CDECHSTD+TSI	300
Sbjct	1267	YMSKAHGIDPNVRTGVRTITTTGASITYSTYKFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA KL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELATKLSTLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETATVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PAIIPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYREFDEMEEC 1711	

>gi|1814088|dbj|BAA09074.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGLFGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCG SDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSDLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSV ATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHS D+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLP CQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+GENLPYLVAIQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQN++TLTHP+TKYIMTCMSADLEVVTSTWVlvvggvlAAL AYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLRYEFDEMEEC 685	
Sbjct	1687	+LSGKPA+IPDRE LY+EFDEMEEC 1711	

> [gi|1160328|dbj|BAA03375.1](#) polyprotein [Hepatitis C virus]

Length=3010

Score = 1225 bits (3170), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240

Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPN+RTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNVRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGINAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVDFSLDPTFTTITET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYD+GCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDSGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAAYQATVCAR+QAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARSQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> [gi|56342203|dbj|BAD73979.1](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLKGS SGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPVSYLKGS SGGPLLCPSGHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+I CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFITACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYQQFDEMEEC 1711	

> gi|56342189|dbj|BAD73972.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVD DLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDLDLVGWQAPSGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPPLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPPLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420

Sbjct	1387	GGRHLIFCHSKKKKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKSGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVlvvggvlaalaaYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVlvvggvlaalaaYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQEFDEMEEC 1711	

> gi|7650252|gb|AAF65957.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLYKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLYKGSSGGPLLCP GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPISYLYKGSSGGPLLCPLGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPNI RTG+RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNIRTGIRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALK ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSALGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRIGIYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTP+ETTVRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPSETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTGSVIVIGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC	1711

> [gi|7650242|gb|AAF65952.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 668/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWPAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP LLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKGS SGGP LLC P+GH VGIFRAAVCTRGVAKAVDFIPVE++ETT+R	
Sbjct	1147	DSRGSLLSPRPVSYLKGS SGGP LLC P SGHIVGIFRAAVCTRGVAKAVDFIPVESMETTIR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPT GSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPT GSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPT GSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVR ITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRAITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AAKL +LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKLSS LGLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ G+YRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMGVYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600

Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSG+PA++PDREVLRY++FDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLRYQQFDEMEEC 1711	

> gi|5918959|gb|AAD56195.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPTCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DGRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFETDSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFETDSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPNIRTG+RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNIRTGIRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSGKPA+IPDREVLRY+EFDEMEEC
 Sbjct 1687 ILSGKPAVIPDREVLRYQEFDEMEEC 1711

> gi|5918943|gb|AAD56187.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
 Identities = 628/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG
 Sbjct 1027 APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHHGAG 1086

Query 61 TRTIASPKGPVIMQYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG
 Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE +ETTMR
 Sbjct 1147 DTRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVEAMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG +PNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAHGTEPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK 1386

Query 361 GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSKKKKDELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSG+PA+IPDREVLRYREFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLRYREFDEMEEC 1711

> gi|27544244|dbj|BAC54896.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSITPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKGS SGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKGS SGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSSLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET++RLRAY+NT PGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSIRL RAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLTRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC	1711

> gi|11559453|dbj|BAB18806.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1225 bits (3169), Expect = 0.0, Method: Composition-based stats.
Identities = 631/685 (92%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ++QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQA PPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPA+IPDREVLY+EFDEMEEC 1711	

> gi|56342243|dbj|BAD73999.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGL GCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	

Sbjct	1087	TKTLAGQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+GEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLŠGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> gi|56342241|dbj|BAD73998.1 polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+GEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

>gi|56342237|dbj|BAD73996.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	

Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSLGLNNAVAYYRGLDVSVIPTSGDV VVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQEFDEMEEC 1711	

>gi|11559461|dbj|BAB18810.1| polyprotein [Hepatitis C virus]
Length=3014

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 632/685 (92%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCING CWTV+HGAG	60
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGACWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLKGS SGGP L LCP GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKGS SGGP L LCP L GHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA SPVF TDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	240
Sbjct	1207	SPVF TDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+G DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS+TGEIPFYGKAIP+EVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSSTGEIPFYGKAIPLEVIK	1386

Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSGKPA+IPDREVL YREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVL YREFDEMEEC 1711	

>gi|221615|dbj|BAA18894.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1224 bits (3168), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY QQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYXQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWHAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAA GYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAA XGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTG PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGVRTITTGGPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSGLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	

Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRGGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLV YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVVYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKFIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSG+PA++PDREVLRYREFDEMEEC	
Sbjct	1687	ILSGRAVVPDREVLRYREFDEMEEC 1711	

>gi|56342239|dbj|BAD73997.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3167), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSRKKCDELAAKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQEFDEMEEC	1711

> gi|1814085|dbj|BAA09071.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1224 bits (3167), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGL GCIIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLFGCIIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCG SDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSV ATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLPSVTATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHS D+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECHSIDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKSLGLNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLP CQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPFCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GENLPYLVAYQATVCARAQAPPPSWDQMWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENLPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQN++TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAAL AYCL+TG VVIVGR+	

Sbjct 1627 RLGAVQNDVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALTAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
+LSGKPA+IPDRE LY+EFDEMEEC

Sbjct 1687 ILSGKPAVIPDREALYQEFDEMEEC 1711

>gi|56342201|dbj|BAD73978.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1224 bits (3166), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG

Sbjct 1027 APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
T+T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG

Sbjct 1087 TKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
DSRGSLLSPRP+SYLGSSGGPLLCP+GHA GIFRAAVCTRGVAKAVDF+PVE++ETTMR

Sbjct 1147 DSRGSLLSPRPVSYLGSSGGPLLCPSGHAAGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 240
SPVFTDNSSPP VPQ+FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA

Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI 300
YMSKAHGIDPNIRTGVRTITTG+PITYSTYKGFLADGGCGSGGAYDIIICDECHSTD+T+I

Sbjct 1267 YMSKAHGIDPNIRTGVRTITTGAPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK

Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
GGRHLIFCHS+KKCDELAACKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG

Sbjct 1387 GGRHLIFCHSRKKCDELAACKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgKPGIYRFVAPGE 480
DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE

Sbjct 1447 DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRTGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT

Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPGLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
HIDAFLSQTQK+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY

Sbjct 1567 HIDAFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV 660
RLGAVQNE+TLTHP+TK+I CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+

Sbjct 1627 RLGAVQNEVTLTHPITKFITACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
+LSGKPA+IPDREVLRY++FDEMEEC

Sbjct 1687 ILSGKPAVIPDREVLRYQQFDEMEEC 1711

> gi|7650264|gb|AAF65963.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1224 bits (3166), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRG+LGCIIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGVLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFOVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+ ITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGASITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGE+PFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEVPFYGKAIPLENIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDMWKCLIRL+PTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDMWKCLIRLRPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		+LSG+PA++PDREVLRYREFDEMEEC	
Sbjct	1687	ILSGRPVVDPDREVLRYREFDEMEEC	1711

> gi|5918941|gb|AAD56186.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1224 bits (3166), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE +ETTMR DTRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVEAMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG +PNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAHGTEPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE DFDSVIDCNTCVTQTVDLSLDPFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVTLTHPITKFIMCMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	+LSG+PA+IPDREVLYREFDEMEEC ILSGRPAVIPDREVLYREFDEMEEC	1711

> [gi|5441842|emb|CAB46917.1|](#) non-structural polyprotein [Hepatitis C virus]
[gi|5441836|emb|CAB46913.1|](#) non-structural polyprotein [Hepatitis C virus]
 Length=1985

Score = 1224 bits (3166), Expect = 0.0, Method: Composition-based stats.
 Identities = 630/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	2	APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	61

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	62	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	121
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	122	DSRGSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	181
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	182	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	241
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	242	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	301
Query	301	LGIGTVLDQAEATAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAEATAGARLVVLATATPPGSVTVPHPNIEEVALS+TGEIPFYGKAIP+E IK	
Sbjct	302	LGIGTVLDQAEATAGARLVVLATATPPGSVTVPHPNIEEVALSSTTGEIPFYGKAIPETIK	361
Query	361	GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAACKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	362	GGRHLIFCHSKKKKCELAACKLSGLGLNAVAYYRGLDVSVIP TSGDVIVVATDALMTGFTG	421
Query	421	DFDSVIDCNTCVTQTQVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTQVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	422	DFDSVIDCNTCVTQTQVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMGIYRFVTPGE	481
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	482	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	541
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	542	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	601
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+T THP+TKYIM CMSADLEVVTTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	602	RLGAVQNEVTTTHPITKYIMACMSADLEVVTTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	661
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAIIPDREVLYREFDEMEEC	
Sbjct	662	ILSGKPAIIPDREVLYREFDEMEEC	686

> gi|56342193|dbj|BAD73974.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1223 bits (3165), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		RT+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	ARTLAGQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	

Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVE\$METTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSCGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSCGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS +GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> gi|11559459|dbj|BAB18809.1 polyprotein [Hepatitis C virus]
Length=3010

Score = 1223 bits (3165), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRPISYLGSSGGPLLCP GH VGIFRAAVCTRGVAKAV+F+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G+DPN+RTGVRTITTTG+PITYSTYGYKFLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA KL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLFEWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G++ PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	+LSG+PAIIPDREVLY+EFDEMEEC	1711

> [gi|56342191|dbj|BAD73973.1](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.
Identities = 628/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrrg	120
Sbjct	1087	T+T+A GP+ QMYTNVD DLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYGYKFLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTGTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQEFDEMEEC 1711	

> [gi|7650224|gb|AAF65943.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.
 Identities = 628/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA QTFLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQTFLATCVNGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVS YLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCGSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTGVRTITTG+PITYSTYGKFLADGGCGSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTGAPITYSTYGKFLADGGCGSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446

Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTI+T T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIDTTTVPQDAVSRTQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		IDAHFLSQTQK+G+N PY+VAYQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	
Sbjct	1567	RIDAHFLSQTQKQAGDNFPYMVAYQATVCARAQAPPPSWDQMWKCLTRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSG+PAIIPDREVL YREFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVL YREFDEMEEC 1711	

>gi|11559465|dbj|BAB18812.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1028	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1088	SKTLAGPKGPITQMYTNVDQDLVGWLAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1147
Query	121	dsrgsllsprPISYLGSSGGPLLC PAGHVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLGSSGGPLLC P+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1148	DGRGSLLSPRPVS YLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1207
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATL FGA	
Sbjct	1208	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLSFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTITTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1268	YMSKAHGTDPNIRTGVRTITTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGE+PFYGKAIP+E IK	
Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEVPFYGKAIPIEAIK	1387
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1388	GGRHLIFCHSKKKCDELA AKLSALGLNAVAYYRGLDVSVIP TNGDVVVVATDALMTGFTG	1447
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1448	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSR+QRRGRTGRGRRGIYRFVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET++RLRAY+NTPGLPVCQDHLEFWEGVFTGLT	

Sbjct	1508	RPSGMFDSSVLCECYDAGCAWYELTPAETSIRLRLAYLNTPLPVCQDHLEFWEGVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1568	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNEI LTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1628	RLGAVQNEIILTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1687
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSG+PA++PDREVLRYREFDEMEEC	
Sbjct	1688	ILSGRPAVVPDREVLRYREFDEMEEC 1712	

>gi|11559443|dbj|BAB18801.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLA+C+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLASCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKGS SGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVS YLKGS SGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG+RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGIRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LGINA+AYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSGLGINAIAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRTQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
 RLGAV NE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVHNEVTLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSG+PA+IPDREVLYREFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLYREFDEMEEC 1711

> [gi|56342229|dbj|BAD73992.1|](#) polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
 Sbjct 1027 APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1087 TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRP+SYLKSSGGPPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
 Sbjct 1147 DSRGSLSPRPVSYLKSSGGPPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKA+G+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAYGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVVATDALMTGYTG 420
 GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSRKKCDELAALKSLGLLNAVAYYRGLDVSVIPTSGDV VVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSGKPAI+PDREVLY+EFDEMEEC

Sbjct 1687 ILSGKPAILPDREVLYQEFDEMEEC 1711

> gi|56342225|dbj|BAD73990.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		+GIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	MGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSLGLLNAVAYYRGLDVSVIP TNGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+PGIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRPGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlyggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMCMSADLEVATSTWVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQQFDEMEEC 1711	

> gi|56342199|dbj|BAD73977.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLPNSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSLGLLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLFEWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLFEWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQQFDEMEEC 1711	

>gi|56342197|dbj|BAD73976.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFETDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCDELA AKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTITET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> gi|56342195|dbj|BAD73975.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1222 bits (3163), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	RT+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	DSRGSLLSPRP+SYLKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS +GEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNSGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLDLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQQFDEMEEC 1711	

> gi|496367|dbj|BAA03905.1| polyprotein precursor [Hepatitis C virus type 2]
Length=2284

Score = 1222 bits (3162), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRGLLGCIITSLTGRDKNQV+GEVQ++STA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	301	APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFATCNGVCWTVYHGAG	360
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSPTCTCGSSDLYLVTRHADVIPVrrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	361	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	420
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VGI FRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	421	DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	480
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLNPSVAATLGFGA	240
Sbjct	481	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVRVLNPSVAATLGFGA	540

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	541	YMSKAHGI+PNIRTGVRTITTTG PITYSTYKFLADGGCSGGAYDIIICDECHSTD T+I	600
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	601	LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+E IK	660
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	661	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	720
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	721	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	780
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWGVFTGLT	540
Sbjct	781	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLFEW VFTGLT	840
Query	541	HIDAHFLSQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	841	HIDAHFLSQTKQ+G+N PYLWAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	900
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVSTWvlvggvlalaaYCLSTGCVVIVGRV	660
Sbjct	901	RLGAVQNEITLTHP+TK++M CMSADLEVVSTWVLVGGVLAALAAAYCL+TG VVIVGR+	960
Query	661	VLSGKPAIIPDREVLVLYREFDEMEEC	685
Sbjct	961	+LSG+PA++PDREVLVLYREFDEMEEC	985

> gi|1749762|dbj|BAA14035.1 unnamed protein product [Hepatitis C virus]
Length=3010

Score = 1222 bits (3162), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQV+GEVQ++STA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYK VLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGI+PNIRTGVRTITTTG PITYSTYKFLADGGCSGGAYDIIICDECHSTD T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLTGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLGAVQNEITLTHP+TK++M CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEITLTHPITKFVMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685 +LSG+PA++PDREVL YREFDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVL YREFDEMEEC 1711	

> [gi|56342227|dbj|BAD73991.1|](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1222 bits (3161), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI VTS LTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAGQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTSGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK +GIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	360
Sbjct	1327	MGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNVGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+PGIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRPGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREVLYQQFDEMEEC 1711	

> [gi|7650226|gb|AAF65944.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1222 bits (3161), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 660/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTVYHGAG	
Sbjct	1027	APITAYSQQTRGMLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGACWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQV HLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVGH LHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE ALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEAALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSGLGLNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> gi|56342209|dbj|BAD73982.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1221 bits (3160), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWLAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DP+IRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGVDPISIRTGVRTITTTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHS+KKCDELAACKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSRKKCDELAACKLSSGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTITETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDLSLDPFTTITET T+PQDAVSR+QRRGRTRGR+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTITETTTVPQDAVSRSQRRGRTRGRMGIIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTQKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626


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Query   601   RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaayYCLSTGCVVIVGRV   660
          RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+
Sbjct   1627   RLGAVQNEVTLTHPITKIFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI   1686

Query   661   VLSGKPAIIPDREVLYREFDEMEEC   685
          +LSGKPA++PDREVLY++FDEMEEC
Sbjct   1687   ILSGKPAVLPDREVLYQQFDEMEEC   1711

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> gi|5918935|gb|AAD56183.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1221 bits (3160), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

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Query    1   APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG   60
          APITAY+QQTRGL GCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
Sbjct   1027   APITAYSQQTRGLFGCIITSLSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG   1086

Query    61   TRTIASPKGPVIMQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg   120
          ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct   1087   SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG   1146

Query   121   dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR   180
          DSRGSLSPRP+SYLGSSGGPLLC+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETMR
Sbjct   1147   DSRGSLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR   1206

Query   181   SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA   240
          SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA
Sbjct   1207   SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA   1266

Query   241   YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI   300
          YMSKAHGIDPN+RTGVRTITTG+ ITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI
Sbjct   1267   YMSKAHGIDPNVRTGVRTITTGASITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI   1326

Query   301   LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK   360
          LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+E IK
Sbjct   1327   LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPETIK   1386

Query   361   GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG   420
          GGRHLIFCHSKKKCDELA KL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG
Sbjct   1387   GGRHLIFCHSKKKCDELATKLSTLGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG   1446

Query   421   DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgKPGIYRFVAPGE   480
          DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
Sbjct   1447   DFDSVIDCNTCVTQTVD FSLDPTFTIETATVPQDAVSRQRRGRTGRGRMGIYRFVTPGE   1506

Query   481   RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT   540
          RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
Sbjct   1507   RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT   1566

Query   541   HIDAFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY   600
          HIDAFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQM KCLIRLKP TLHGPTPLLY
Sbjct   1567   HIDAFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMLKCLIRLKP TLHGPTPLLY   1626

Query   601   RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaayYCLSTGCVVIVGRV   660
          RLGAVQNEITLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
Sbjct   1627   RLGAVQNEITLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI   1686

Query   661   VLSGKPAIIPDREVLYREFDEMEEC   685

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+LSG+PAIIPDREVLVREFDEMEEC
 Sbjct 1687 ILSGRPAIIPDREVLVREFDEMEEC 1711

> gi|56342215|dbj|BAD73985.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIVTSLSLTGRDKNQVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSL PCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLIPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLSSLGLNAVAYYRGLDVSVIPITSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTITET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTITETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL+AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLIAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+ G VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTAGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685	
		+LSGKPAI+PDREVLV++FDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLVQQFDEMEEC 1711	

> gi|56342211|dbj|BAD73983.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 666/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIVTSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DP+IRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPSIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSSGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRMG IYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAVLPDREVLYQQFDEMEEC 1711	

>gi|7650238|gb|AAF65950.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	

Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg +T+A PKGP+ QMYTNVDQDLVGW +P G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	AKTLAGPKGPITQMYTNVDQDLVGWQSPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGI+P+IRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIEPSIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LG+GTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	360
Sbjct	1327	LGVGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNAGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKSGLGLNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaalaaYCLSTGCVVIVGRV RLGA+QNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGALQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQEFDEMEEC 1711	

>gi|31980453|dbj|BAC77767.1| NS protein [Hepatitis C virus]
Length=1984

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
Identities = 630/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	61	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	120

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	D+RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	181	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKA P+E IK	360
Query	361	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKKCELA KL ALGINAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	420
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLFEWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLFEW VFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVT KYIMTMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	601	RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	660
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	661	+LSGKPA+IPDREVLY+EFDEMEEC 685	

> gi|1814086|dbj|BAA09072.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKS KVP YAAQGYKVLVNLNPSVAATLGFGA	

Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GSKSNKVPVEYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTY GKLADGGCSGGAYDIIICDECHSTD+TSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTV PPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTV PPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPV QDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
Sbjct	1687	+LSGKPAIIPDREVL YREFDEMEEC 1711	

>gi|56342231|dbj|BAD73993.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1221 bits (3158), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G+DPNIRTGVRTITTTG+PITYSTY GKLADGGCSGGAYDIIICDECHSTD+T+I	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCDELAALKSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685.	
		+LSGKPAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAILPDREVLYQEFDEMEEC 1711	

>gi|7650230|gb|AAF65946.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1221 bits (3158), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPrrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G DPNIRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T++	
Sbjct	1267	YMSKAYGTDPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTV	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	

Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRG+TGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGKTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWV LVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWV LVGGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSGKPA+IPDREVL YREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVL YREFDEMEEC 1711	

> [gi|221611|dbj|BAA14233.1](#) unnamed protein product [Hepatitis C virus]
[gi|130469|sp|P26662|POLG_HCVJA](#) Genome polyprotein [Contains: Core protein p21 (Capsid C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
 Length=3010

Score = 1221 bits (3158), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQV+GEVQ++STA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADV+PVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPTCTCGSSDLYLVTRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGI+PNIRTGVRTITTTG PITYSTY KFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIEPNIRTGVRTITTTGGPITYSTYCKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420

Sbjct	1387	GGRHLIFCHSKKKKCELAACL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG GGRHLIFCHSKKKKCELAACL TGLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSR QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRAQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+NLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNLPLYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSG+PA+IPDREVLRY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLRYQEFDEMEEC 1711	

> gi|1181832|gb|AAA86907.1| polyprotein
Length=3010

Score = 1221 bits (3158), Expect = 0.0, Method: Composition-based stats.
Identities = 629/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPVTQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGS GK+TKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKTTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPH NIEEVALS GEIPFYGKAIPLE IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHSNIEEVALSNIGEIPFYGKAIPLENIK	1386
Query	361	GGRHLIFCHSKKKKCELAACLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHS+KKCELAACL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSRKKKCELAACL SGLGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCN CVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNVCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMG IYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCE YDAGCAWYELTPAE +VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCE SYDAGCAWYELTPAEASVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TGCVVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKIFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGCVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAI+PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIVPDREVLYQEFDEMEEC 1711	

> [gi|4753719|emb|CAB41950.1|](#) polyprotein [Hepatitis C virus]
 Length=3012

Score = 1220 bits (3157), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1029	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLV+RHADVIPVRRRG	
Sbjct	1089	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSLTPCTCGSSDLYLVSRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETT R	
Sbjct	1149	DSRGSLSPRPVSYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVEMETTTR	1208
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1209	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DP+IRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1269	YMSKAHGVDPSIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I+	
Sbjct	1329	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIR	1388
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAL+L LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1389	GGRHLIFCHSKKKCDELAALQSLGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1448
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgryKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTRGR+ GIYRFV PGE	
Sbjct	1449	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTRGRGRIYRFVTPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600

Sbjct	1569	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV RLGAVQNE+TLTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1629	RLGAVQNEVTLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1688
Query	661	VLSGKPAIIPDREVLVREFDEMEEC 685 +LSGKPAI+PDR VLYREFDEMEEC	
Sbjct	1689	ILSGKPAIVPDRGVLYREFDEMEEC 1713	

> gi|56342221|dbj|BAD73988.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1220 bits (3157), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TKTLAGQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DP+IRTGVRT+TTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAHGVDPSIRTGVRTVTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP+ETIK	1386
Query	361	GGRHLIFCHSKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCELAALK LG+NAVAYYRGLDVS+IP GDVVVVATDALMTG+TG GGRHLIFCHSRKKCELAALKSLGLNAVAYYRGLDVSIIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCV QTVDVSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE DFDSVIDCNTCVIQTVDVSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWEVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVTLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686

Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSGKPAI+PDREVLV++FDEMEEC
 Sbjct 1687 ILSGKPAIVPDREVLVQQFDEMEEC 1711

>gi|56342217|dbj|BAD73986.1| polyprotein [Hepatitis C virus type 1b]
 Length=3010

Score = 1220 bits (3157), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
 Sbjct 1027 APITAYAQQTRGLLGCIVTSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 T+T+AS KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1087 TKTLASQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D+RGSLLSPRPISYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR
 Sbjct 1147 DNRGSLLSPRPISYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR 1206

Query 181 SPVFTDNSSPPVPVQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG++PNIRTGVRTITTG+PITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAHGVEPNIRTGVRTITTGAPITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK 1386

Query 361 GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKCE+AAKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSKKKKCEVAALKSLGLNNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRQRRGRTGRGRTGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKP LHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPV LHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+ THP+TKYIMTCM+ADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVIFTHPITKYIMTCMAADLEVATSTWVLVGGVLAALAAAYCLTTG SVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSGKPAI+PDREVLV++FDEMEEC
 Sbjct 1687 ILSGKPAIVPDREVLVQQFDEMEEC 1711

> gi|56342213|dbj|BAD73984.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1220 bits (3156), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSL PCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLIPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP IETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSSGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD SLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDLSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL+AYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLIAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+ G VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITK FIMACMSADLEVATSTWVLVGGVLAALAAAYCLTAGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	I LSGKPAIVPDREVLYQQFDEMEEC	1711

> gi|221605|dbj|BAA02756.1| polyprotein precursor [Hepatitis C virus]
Length=3010

Score = 1220 bits (3156), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRG+LGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YM KAHGIDPNIRTGVRTITTTG PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIPPIGDV VVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSVLCCEYDAGCAWYELTPAETT VRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSVLCCEYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGL+	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	+LSGKPA++PDREVLY+EFDEMEEC	1711

> gi|1814087|dbj|BAA09073.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1220 bits (3156), Expect = 0.0, Method: Composition-based stats.
 Identities = 627/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	

Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTM	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTG RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGARTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP L IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP LDTIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG	420
		GGRHLIF HSKKKKCELA KL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFWHSKKKKCELA TKLSALGVNAVAYYRGLDVSVIP TSGNVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCV QTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVIQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		R SGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RTSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

> gi|18027685|gb|AAL55821.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1219 bits (3155), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCI VTS LTGRDKNQVEGEVQV VSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAGQKGPITQMYTNVDQDLVGWLAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTM	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTITETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTTITET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

>gi|7650250|gb|AAF65956.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1219 bits (3155), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETT R	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct		YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+TSI	

Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLLNAVAYYRGLDVSVIPVSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		D DSVIDCNCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DLDSVIDCNCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTQKSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTQK+G+NLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTQKAGDNL PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVVPDREVLYREFDEMEEC	1711

> gi|11559467|dbj|BAB18813.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1219 bits (3155), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 664/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSF LATCINGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGP L LCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGP L LCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYA QGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYATQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G+DPN+RTGVRT+TTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGMDPNLRTGVRTVTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK	1386

Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGLNAVAYYRGLDVSVIPTSGDV VVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		+FDSVIDCNTCV QTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	NFDSVIDCNTCVNQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYQEFDEMEEC 1711	

> gi|11559463|dbj|BAB18811.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1219 bits (3155), Expect = 0.0, Method: Composition-based stats.
 Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DS+GSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSKGSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+G+DPNIRTGVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGVDPNIRTGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEV LS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVGLSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAAL+L++LG+NAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAARLLSLGVNAVAYYRGLDVSVIPTSGDV VVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	

Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWD MWKCL RLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDLMWKCLTRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVVLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSG+P IIPDREVL YREFDEMEEC	
Sbjct	1687	ILSGRPVIIPDREVL YREFDEMEEC 1711	

>gi|56342205|dbj|BAD73980.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1219 bits (3154), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGL GCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLFGCIVTSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLT PCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKQGPITQMYTNVDQDLVGWQAPPGARSLT PCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVPVQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDP+IRTGVRTITTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPSIRTGVRTITTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP IETIK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA KL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELA EKLSLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRTGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTK+I CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPVTKFITACMSADLEVATSTWVLVGGVLAALAAAYCLTTGGSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQQFDEMEEC	1711

> [gi|385584|gb|AAB27127.1|](#) polyprotein [Hepatitis C virus]

[gi|743453|prf|12012309A](#) polyprotein

Length=3014

Score = 1218 bits (3152), Expect = 0.0, Method: Composition-based stats.
Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAAQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY++QTRGLLGCIITS LTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSRRQTRGLLGCIITS LTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPIAQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKGS SGGP L LCP+GHAVG+FRFAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DNRGSLLSPRPVS Y LKGS SGGP L LCPSGHAVGVFRFAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVF TDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF TD SSPP VPQ+FQVAHLHAPTGS GKST+VPAAYA QGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVF TD TSSPPAVPQT FQVAHLHAPTGS GKSTRVPAAYATQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTIT TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTGVRTIT TG+PITYSTY GKFLADGGCSGGAYDII+CDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGVRTIT TGAPITYSTY GKFLADGGCSGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIM	1386
Query	361	GGRHLIFCHSKKKCDELA AKL VALGINAVAYYRGLDVSVIPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLSGLGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQT VDFSLDPTFTIETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQT VDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQT VDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDS VLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSPVLCECYDAGCAWYELTPAETSRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660

Sbjct 1627 RLGAVQNE+TLTHP+TKYIM CM ADLEVVSTWVLVGGVLAALAAAYCL+TG VVIVGR+ 1686
 RLGAVQNEVTLTHPITKYIMACMWADLEVVSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI
 Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSG+PA++PDREVLVREFDEMEEC
 Sbjct 1687 ILSGRPAVVPDREVLVREFDEMEEC 1711

>gi|560789|dbj|BAA06303.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1218 bits (3151), Expect = 0.0, Method: Composition-based stats.
 Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG
 Sbjct 1027 APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVFHHGAG 1086
 Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLVLRHADVIPV RRG
 Sbjct 1087 SKTLAGEPKGPITQMYTNVDQDLVGSAPPGARSLTPCTCGSSDLVLRHADVIPVHRRG 1146
 Query 121 dsrgsllsprPISYLKSSSGGPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSP PISYLKSSSGGPL CP+G VGIFRAAVCTRGVAKAVDF+PVE++ETMR
 Sbjct 1147 DSRGSLSPGPISYLKSSSGGPLPCPSGRVVGIFRAAVCTRGVAKAVDFVPVESMETMR 1206
 Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTDNS+PP VPQ+FQVAHLHAPTGSKGST+VPAAYAAQGYKVLVNLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSTPPAVPQTFQVAHLHAPTGSKGSTRVPAAYAAQGYKVLVNLNPSVAATLGFGA 1266
 Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI
 Sbjct 1267 YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI 1326
 Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIPLE IK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEAIK 1386
 Query 361 GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG 420
 GGRHLIFCHSKKKKDELAALKL ALG+NAVAYYRGLDVS+IP GDV VVVATDALMTGYTG
 Sbjct 1387 GGRHLIFCHSKKKKDELAALKLSALGVNAVAYYRGLDVSIIPTSGDV VVVATDALMTGYTG 1446
 Query 421 DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRGGIYRFVTPGE 1506
 Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566
 Query 541 HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
 HIDAHFLSQTKQ+G+N PYLVAQATVCARA+APPPSWDMWKCLIRLKP TLHGPTPLLY
 Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVAQATVCARAKAPPPSWDMWKCLIRLKP TLHGPTPLLY 1626
 Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVSTWVlvvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TK+IM CMSADLEVVSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVTLTHPITKFIMACMSADLEVVSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686
 Query 661 VLSGKPAIIPDREVLVREFDEMEEC 685
 +LSG+PA+IPDREVLV+EFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLVQEFDEMEEC 1711

> gi|56342219|dbj|BAD73987.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1217 bits (3149), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIMQMYTNVDQDLVGWPAPQGSRSITPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG++PNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGVEPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS+KKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSRKKCELAALKSLGLNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKP LHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPVLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
		RLGAVQNE+ THP+TK+IMTCM+ADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVIFTHPITKFIIMTCMAADLEVATSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQQFDEMEEC 1711	

> gi|3098633|gb|AAC15722.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1217 bits (3149), Expect = 0.0, Method: Composition-based stats.

Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNS+PP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALK LG+NAVAYYRGLDVSVIPPIGDV VVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	+LSGKPA++PDREVLY+EFDEMEEC	1711

> gi|86372255|gb|ABC95195.1| polyprotein [Hepatitis C virus]
 Length=3014

Score = 1217 bits (3149), Expect = 0.0, Method: Composition-based stats.
 Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1031	APITAYAQQTRGLLGCI+TSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1090

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGPV QMYTNVDQDLVGWPAP G+RSLT CTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1091	SKTLAGPKGPVTQMYTNVDQDLVGWPAPPGARSLTACTCGSSDLYLVTRHADVIPVRRRG	1150
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+S LKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1151	DSRGSLLSPRPLSNLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1210
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPV+TDNSSPP VPQ+FQVA+LHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1211	SPVYTDNSSPPAVPQTFQVAYLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1270
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1271	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1330
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1331	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETIK	1390
Query	361	GGRHLIFCHSKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHL FCHSKKKCELAALKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1391	GGRHLTFCHSKKKCELAALKSSLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1450
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1451	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1510
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1511	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1570
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1571	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1630
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggylaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVI GR+	
Sbjct	1631	RLGAVQNEVTLTHPMTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSVVIAGRI	1690
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1691	ILSGRPAVVPDREVLYREFDEMEEC 1715	

> gi|67773303|gb|AA81920.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1217 bits (3148), Expect = 0.0, Method: Composition-based stats.
 Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	

Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYTGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYTGKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYTGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS+TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSSTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKSLGLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRMGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+T THP+TKYIM CM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTTTHPITKYIMACMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAIIPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYREFDEMEEC 1711	

>gi|56342223|dbj|BAD73989.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1217 bits (3148), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIIVTSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg	120
		T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLVLRHADVIPVRRRG	
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLVLRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+P E +ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPAEAMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ++QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQAYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G+DPNIRTGVRT+TTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHS+KKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCV QTVDLSLPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDREVLY++FDEMEEC 1711	

> [gi|221607|dbj|BAA01583.1](#) polyprotein precursor [Hepatitis C virus]
Length=3010

Score = 1217 bits (3148), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRP+SYLKSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG GSITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDIVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLTGLGLNAVAYYRGLDVSVIPPIGDIVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNCVTQTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNCVTQTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685 +LSGKPA++PDREVLRY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLRYQEFDEMEEC 1711	

> gi|80322852|gb|ABB52628.1| polyprotein [Hepatitis C virus]
Length=2314

Score = 1216 bits (3147), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	354	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	413
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Sbjct	414	SKTLAGPKGPITQMYTNVDQDLVGWPAPSGARSRLTPCTCGSSDLYLVRHADVIPVRRRG	473
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+RGSLLSPRPISYLKSSGGPLLCP+GH GIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	474	DNRGSLLSPRPISYLKSSGGPLLCPSGHVAGIFRAAVCTRGVAKAVDFVPVESMETTMR	533
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTK PAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	534	SPVFETDNSSPPAVPQTFQVAHLHAPTGSGBKSTKAPAAAYAAQGYKVLVLNPSVAATLGFGA	593
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDEC TD+TSI	300
Sbjct	594	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIMCDECRPTDSTSI	653
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E K	360
Sbjct	654	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPETTK	713
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDIVVVVATDALMTGYTG GGR+LIFCHSKKKKCELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	714	GGRYLIFCHSKKKKCELAALKLSALGINAVAYYRGLDVSVIPTSGDIVVVVATDALMTGYTG	773

Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	774	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	833
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	834	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	893
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCL+RLKP TLHGPTPLLY	
Sbjct	894	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLMRLKP TLHGPTPLLY	953
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIMTCM+ADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	954	RLGAVQNEVTLTHPITKYIMTCMAADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1013
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PA IPDREVLYREFDEMEEC	
Sbjct	1014	ILSGRPATIPDREVLYREFDEMEEC	1038

>gi|5918963|gb|AAD56197.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1216 bits (3146), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHHAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLC PAVHAGVIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLC P+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVS YLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCGSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG RTITTTG+PITYSTYGKFLADGGCGSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGARTITTTGAPITYSTYGKFLADGGCGSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYG+AIIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGRAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GRHLIFCHSKKKCDELA AKL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	EGRHLIFCHSKKKCDELA AKLSALGLNAVAYYRGLDVSVIP TSGNVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQN++TLTHP+TK IM CMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNDVTLTHPITKLIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRL	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> gi|5918961|gb|AAD56196.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1216 bits (3146), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGARTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYG+AIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGRAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAACLVALGINAVAYYRGLDVSVIPPIGDDVVVATDALMTGYTG	420
		GRHLIFCHSKKKCDELAACL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	
Sbjct	1387	EGRHLIFCHSKKKCDELAACLALGLNAVAYYRGLDVSVIP TSGNVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626

Query 601 RLGA VQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV 660
 RLGA VQN++TLTHP+TK IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGA VQNDVTLTHPITKLIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRL 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSG+PA+IPDREVLYREFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLYREFDEMEEC 1711

> [gi|1944376|dbj|BAA19625.1](#) unnamed protein product [Hepatitis C virus]
 Length=3010

Score = 1216 bits (3145), Expect = 0.0, Method: Composition-based stats.
 Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG
 Sbjct 1027 APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVFHGAG 1086

Query 61 TRTIASPKGPVIMQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVDQDLVGW AP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRP+SYLKSSGGPL CP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR
 Sbjct 1147 DSRGSLSPRPVSYLKSSGGPLPCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 1206

Query 181 SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 +PVFTDNSSPP VPQ+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
 Sbjct 1207 APVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKA+G DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+T+I
 Sbjct 1267 YMSKAYGTDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIMCDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGT LDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK
 Sbjct 1327 LGIGTALDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLEVIK 1386

Query 361 GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSKKKKDELAALKLSTLGLNAVAYYRGLDVSVIP TSGDVVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLEFWE VFTGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT 1566

Query 541 HIDA HFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDA HFLSQTKQ+G+N PYLVA YQATVCARAQA PPSWDQMWKCL RLKPTLHGPTPLLY
 Sbjct 1567 HIDA HFLSQTKQAGDNFPYLVA YQATVCARAQASPPSWDQMWKCLRLKPTLHGPTPLLY 1626

Query 601 RLGA VQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV 660
 RLGA VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGA VQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSGKPA+IPDREVLYREFDEMEEC

Sbjct 1687 ILSGKPAVIPDREVLRYREFDEMEEC 1711

> gi|1814089|dbj|BAA09076.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1216 bits (3145), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 657/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTATQSFATCTNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGSKGPITQMYTNVDQDLVGWQAPSGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGS KVP YAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKSNKVPVEYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLGINAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLPTFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLPTFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPV QDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVPWQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlyvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLYVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLYVGGVLAALAAAYCLTTSVIVVIGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLRYREFDEMEEC 1711	

> gi|19568933|gb|AAL91977.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1215 bits (3144), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC++G CWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPEGHAGVIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPEGHAGVIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFDTNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFDTNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATL FGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG++PNIRTGVRT+TTG+ ITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VR+RAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	R+GAVQNE+ LTHPVTKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+LSGKPAIIPDRE LY+ FDEMEEC 1711	

>gi|56342235|dbj|BAD73995.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1215 bits (3144), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG GGRHLIFCHSKKKCDELAALKLSGLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCN CVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTRGRG+ G YRFV PGE DFDSVIDCNVCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTRGRGTGT YRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlgvgvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVVLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLREFDEMEEC 685	
Sbjct	1687	+LSGKPAI+PDRE LY++FDEMEEC ILSGKPAIVPDREALYQQFDEMEEC 1711	

> gi|56342233|dbj|BAD73994.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1215 bits (3144), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1147	DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDF+PVE++ETTMR DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGVDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNIGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLNAVAYYRGLDVSVIPTSGDV VVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTITETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCN CVTQTVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ G YRFV PGE	480
Sbjct	1447	DFDSVIDCNVCVTQTVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRTGT YRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvvlvggvlalaaYCLSTGCVVIVGRV RLGAVQNE+ LTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVVLTHPITKFIMACMSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685 +LSGKPAI+PDRE LY++FDEMEEC	
Sbjct	1687	ILSGKPAIVPDREALYQQFDEMEEC 1711	

>gi|3098637|gb|AAC15724.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1215 bits (3144), Expect = 0.0, Method: Composition-based stats.
Identities = 621/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRG+LGC+ITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGVLCVITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAW+ELTPAET+VRLRAY+NTPGLPVCQDHLFEW VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
Sbjct	1687	+LSGKPA++PDREVLRY+EFDEMEEC 1711	

> [gi|15487694|gb|AAL00900.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1214 bits (3142), Expect = 0.0, Method: Composition-based stats.
Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RGSLSPRP+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFG	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+G+DPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDII+CDECHSTD+T++	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ALS TGEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIALSNTGEIPFYGKAIPETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE D DSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DSDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDMWK LIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDMWKS LIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLG VQ+EITLTHPVTKYIM CMSADLEVVTSTWVLV GVLAAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGTQVQSEITLTHPVTKYIMACMSADLEVVTSTWVLVSGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

> [gi|3098635|gb|AAC15723.1|](#) polyprotein [Hepatitis C virus]
Length=3010

Score = 1214 bits (3141), Expect = 0.0, Method: Composition-based stats.
Identities = 620/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY+QQTRG+LGC+ITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYSQQTRGVLCVITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg ++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWAPPGARSMTPPCSCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ+ QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQTSQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTG ITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGGSITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446

Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NT PGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWV VGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVPVGGVLAALAAAYCLTTG SVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC	1711

> gi|3098651|gb|AAC15730.1| polyprotein [Hepatitis C virus]
Length=2864

Score = 1214 bits (3140), Expect = 0.0, Method: Composition-based stats.
Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGC+ITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGV LGCVITSLTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPP GARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGP L LCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVS YLKSSGGP L LCPSGHVVG FRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	240
		SPVF TDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	
Sbjct	1207	SPVF TDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTIT TGGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTIT TGG ITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTIT TGG SITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPG SVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPG SVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPG SVTVPHPNIEEIGLSNNGEIPFYGKAIP IEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540

Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaayCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+ RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

> gi|3098648|gb|AAC15729.1| polyprotein [Hepatitis C virus]
Length=2864

Score = 1213 bits (3139), Expect = 0.0, Method: Composition-based stats.
Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG APITAYSQQTRGVLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR DSRGSLLSPRPVS YLGSSGGPLLCPSGHVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFTDNS+PP VPQ+FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA SPVFTDNSTPPAVPQTFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTG ITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAHGIDPNIRTGVRTITTTGGSITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG GGRHLIFCHSKKKCDELA AKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRGTGRG+ GIYRFV PGE DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRGTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAQVNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685
 +LSGKPA++PDREVLY+EFDEMEEC
 Sbjct 1687 ILSGKPAVVPDREVLYQEFDMEEC 1711

> gi|15529111|gb|AAK97744.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1213 bits (3138), Expect = 0.0, Method: Composition-based stats.
 Identities = 626/685 (91%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG
 Sbjct 1027 APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFATCVNGACWTVFHGAG 1086

Query 61 TRTIASEPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 ++T+A PKGP+ QMYTNVD DLVGW AP GSRSLTPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1087 SKTLAGPKGPITQMYTNVDL DLVGWQAPPGSRSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRP+SYLKSSGGPPLCP+ HAVGIFRAAVCTRGVAKAVDFIPVE++ETMR
 Sbjct 1147 DSRGSLSPRPVSYLKSSGGPPLCPSRHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR 1206

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
 Sbjct 1207 SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHGIDPNIRTGVR ITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I
 Sbjct 1267 YMSKAHGIDPNIRTGVRAITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS GEIPFYGKAIP+EVIK
 Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNAGEIPFYGKAIPIEVIK 1386

Query 361 GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG 420
 GGRHLIFCHSKKK DELAAKL ALG+NAVAYYRGLDVSVIP GDV VVVATDALMTG+TG
 Sbjct 1387 GGRHLIFCHSKKKYDELAALKLSALGLNAVAYYRGLDVSVIP TNGDV VVVATDALMTGFTG 1446

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAV+R+QRRGRTGRG+ GIYRFV PGE
 Sbjct 1447 DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVARSQRRGRTGRGRRGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE V TGLT
 Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVSTGLT 1566

Query 541 HIDAFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY
 Sbjct 1567 HIDAFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV 660
 RLGAQVNEITLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1627 RLGAVQNEITLTHPMTKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLYREFDEMEEC 685

+LSG+PA+IPDREVLYREFDEMEEC
 Sbjct 1687 ILSGRPAVIPDREVLYREFDEMEEC 1711

> gi|3098644|gb|AAC15727.1| polyprotein [Hepatitis C virus]
 Length=2864

Score = 1213 bits (3138), Expect = 0.0, Method: Composition-based stats.
 Identities = 622/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGCIITSLSLTGRDKNQVEGEVQ+VSTA +FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLGCIITSLSLTGRDKNQVEGEVQVVSTATHSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLEGSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG IITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET T+PQDAVSR+QRRGRGTGRG+ GIYRFV+PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTVPQDAVSRSQRRGRGTGRGRSGIYRFVSPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

> gi|3098639|gb|AAC15725.1| polyprotein [Hepatitis C virus]
 Length=3010

Score = 1213 bits (3138), Expect = 0.0, Method: Composition-based stats.
Identities = 621/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGC ITS LTGRDKNQVEGEVQ+VSTA +FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLGXCITS LTGRDKNQVEGEVQVVSTATXSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLPSPGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG IYTYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELAALK LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

>gi|1814090|dbj|BAA09075.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1212 bits (3136), Expect = 0.0, Method: Composition-based stats.
Identities = 624/685 (91%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	

Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRP+SYLKGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	180
Sbjct	1147	DSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA SPVFETDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTG RTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	300
Sbjct	1267	YMSKAHGVDPNIRTGARTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+ IK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPLDTIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIF HSKKKCDELA KL ALG+NAVAYYRGLDVSVIP G+VVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFWHSKKKCDELATKLSALGVNAVAYYRGLDVSVIPTSGNVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE DFDSVIDCNTCV QT DFSLDPFTTETIET.T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	480
Sbjct	1447	DFDSVIDCNTCVIQTDDFSLDPFTTETIETRTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT R SGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RTSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPRTLHGPTPLLY HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCL RLKPRTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLTRLKPRTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlalaayCLSTGCVVIVGRV RLGAVQNE+ LTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	660
Sbjct	1627	RLGAVQNEVILTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 +LSGKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGKPAVIPDREVLYREFDEMEEC 1711	

> [gi|56342207|dbj|BAD73981.1|](#) polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1212 bits (3135), Expect = 0.0, Method: Composition-based stats.
Identities = 619/685 (90%), Positives = 657/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGL GCI+TSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg T+T+A KGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTR+ADVIPVRRRG	120
Sbjct	1087	TKTLAQKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRYADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGH AVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKGSSGGP L LCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKGSSGGP L LCPSGH AVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIP IETIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA KL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELA VKLSSLGLNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+Q RGRTG G G+YRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQLRGRTGSGTTGMYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		R SGMFDSSVLCECYDAGC WYELTPAET+VRLRAY+N PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RTSGMFDSSVLCECYDAGCTWYELTPAETS VRLRAYLNAPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		IDAHF+SQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	KIDAHFMSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEV TSTWVLVGGVLAALAAAYCL+TG VVIVGRV	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACSADLEVATSTWVLVGGVLAALAAAYCLTTGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAI+PDREVLY++FDEMEEC	
Sbjct	1687	ILSGRPAIVPDREVLYQQFDEMEEC 1711	

>gi|3098646|gb|AAC15728.1| polyprotein [Hepatitis C virus]
Length=2864

Score = 1212 bits (3135), Expect = 0.0, Method: Composition-based stats.
Identities = 621/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGC+ITS LTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGV LGCVITS LTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYL VTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYL VTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDL DLVGWQAPP GARSMTPCSCGSSDLYL VTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGH AVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKGSSGGP L LCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKGSSGGP L LCPSGH VVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	

Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGGSITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVFLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVFLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVFLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAW+ELTPAET+VRLRAY+NTPGLPVCQDHLFEWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWHELTPAETSVRLRAYLNTPLPVCQDHLFEWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlgvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPA++PDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLYQEFDEMEEC 1711	

> [gi|59479|emb|CAA43793.1|](#) JK1-full [Hepatitis C virus]
 Length=3010

Score = 1211 bits (3134), Expect = 0.0, Method: Composition-based stats.
 Identities = 626/685 (91%), Positives = 658/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGL GCI+TSLTGRDKNQVEGE Q+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLFGCIVTSLTGRDKNQVEGEAQVVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+ SLTPCT GSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPINQMYTNVDQDLVGWQAPSGAASLTPCTYGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNI TGVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPNISTGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLA ATPPGSVTVPHPNIEEVAL TGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLAATPPGSVTVPHPNIEEVALPNTGEIPFYGKAIPLETIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLSALGVNAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET TLPQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTLPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPA T+VRLRAY+NTPGLPVCQ HLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSSVLCECYDAGCAWYELTPAVTSVRLRAYLNTPLPVCQVHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAIIPDREVLYQEFDEMEEC 1711	

>gi|3810874|dbj|BAA20975.1| precursor polyprotein [Hepatitis C virus]
Length=1186

Score = 1211 bits (3134), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQV+GEVQ++STA Q+FLATC+NGVCWTVYHGAG	
Sbjct	305	APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFLATCVNGVCWTVYHGAG	364
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RS+TPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	365	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPTCTCGSSDLYLVTRHADVIPVRRRG	424
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLC+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	425	DSRGSLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	484
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	485	SPVFETDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	544
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGI+PNIRTGVRTITTTG PITYSTY KFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	545	YMSKAHGIEPNIRTGVRTITTTGGPITYSTYCKFLADGGCSGGAYDIIICDECHSTDSTTI	604
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGS+TVPHPNIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	605	LGIGTVLDQAETAGARLVVLATATPPGSITVPHPNIEEVALSNTGEIPFYGKAIPIEAIK	664
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	

Sbjct	665	GGRHLIFCHSKKKCDELAACKLTGLGLNAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTG	724
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSR QRRGRTGRG+ GIYRFV PGE	
Sbjct	725	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRAQRRGRTGRGRSGIYRFVTPGE	784
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	785	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNT PGLPVCQDHLEFVESVFTGLT	844
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	845	HIDAHFLSQTKQAGDNFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	904
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK++M CMSADLEVVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	905	RLGAVQNEITLTHPITKFVMACMSADLEVVVTSTWVLVGGVLAALAAAYCLTTGSVVIVGRI	964
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSG+PA++PDREVL YREFDEME C	
Sbjct	965	ILSGRPAVVPDREVL YREFDEMEAC 989	

> gi|3098653|gb|AAC15731.1| polyprotein [Hepatitis C virus]
 Length=2864

Score = 1211 bits (3132), Expect = 0.0, Method: Composition-based stats.
 Identities = 621/685 (90%), Positives = 660/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		A ITAY+QQTRG+LGC+ITS LTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	ASITAYSQQTRGV LGCVITS LTGRDKNQVEGEVQVVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPP GARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKGSSGGPLLCPSGHVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAACKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAACKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506

Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC 685	
		+LSGKPA++PDREVLRY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLRYQEFDEMEEC 1711	

> gi|3098642|gb|AAC15726.1| polyprotein [Hepatitis C virus]
 Length=2864

Score = 1210 bits (3131), Expect = 0.0, Method: Composition-based stats.
 Identities = 620/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRG+LGC+ITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYSQQTRGVLGCVITSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLVLVGWQAPPGARSMTPPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLGSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKGSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+ QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTSQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYGKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYGKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	

Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWV VGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVPVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYEFDEMEEC	685
		+LSGKPA++PDREVLRY+EFDEMEEC	
Sbjct	1687	ILSGKPAVVPDREVLRYQEFDEMEEC	1711

> gi|3098655|gb|AAC15732.1| polyprotein [Hepatitis C virus]

Length=2864

Score = 1210 bits (3130), Expect = 0.0, Method: Composition-based stats.

Identities = 620/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APIT Y+QQTRG+LGCIIITSLTGRDKNQVEGEVQ+VSTA +FLATCINGVCWTVYHGAG	
Sbjct	1027	APITTYSSQTRGVLGCIITSLTGRDKNQVEGEVQVVSTATHSFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVD DLVGW AP G+RS+TPC+CGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDLDLVGWQAPPGARSMTPCSCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVVGVFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQV HLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVVHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGGSITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE+ LS GEIPFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEIGLSNNGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKL LG+NAVAYYRGLDVSVIPPIGDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAAKLTGLGLNAVAYYRGLDVSVIPPIGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV+PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRSGIYRFVSPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+ LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVILTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSGKPA++PDREVLRY+EFDEMEEC
 Sbjct 1687 ILSGKPAVVPDREVLRYQEFDEMEEC 1711

> gi|80322850|gb|ABB52627.1| polyprotein [Hepatitis C virus]
 Length=2383

Score = 1209 bits (3127), Expect = 0.0, Method: Composition-based stats.
 Identities = 620/685 (90%), Positives = 661/685 (96%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG
 Sbjct 423 APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVYHGAG 482

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 ++T+A PKGP+IQMYTNVDQDLVGW AP G+RSLTPCTCGSSD YLVTRHADVIPVRRRG
 Sbjct 483 SKTLAGPKGPPIQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDPYLVTRHADVIPVRRRG 542

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D RGSLLSP+PISYLGSSGGPLLCP+GHAVGIFRAAVCTRG+AKAVDF+P E +ETTMR
 Sbjct 543 DGRGSLLSPKPIISYLGSSGGPLLCPSGHAVGIFRAAVCTRGIKAVDFVPAECMETTMR 602

Query 181 SPVFTDNSSPPVPVQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTD+SSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATL FGA
 Sbjct 603 SPVFTDHSSPPTVPQTFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVNLNPSVAATLSFGA 662

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHG+DPNIRTG+RTITTG+PITYSTYKGFLADGGCSGGAYDII+CDECHSTD+T++
 Sbjct 663 YMSKAHGVDPNIRTGMRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTV 722

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+EVIK
 Sbjct 723 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEVIK 782

Query 361 GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKCELAALKL LG+NAV YYRGLDVSVIP GDVVVVATDALMTGYTG
 Sbjct 783 GGRHLIFCHSKKKKCELAALKSLGLNAVYYRGLDVSVIPTSGDVVVVVATDALMTGYTG 842

Query 421 DFDSVIDCNCVQTQTVDFSLDPTFTTITETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE 480
 DFDSVIDCNCVQTQTVDFSLDPTFTT+T T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE
 Sbjct 843 DFDSVIDCNCVQTQTVDFSLDPTFTTIDTTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE 902

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT
 Sbjct 903 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT 962

Query 541 HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
 HIDAH LSQTK +G+N PYLVAAYQATVCARAQAPPPSWDMWKCL+RLKP TLHGPTPLLY
 Sbjct 963 HIDAHLLSQTKDAGDNYPYLVAAYQATVCARAQAPPPSWDMWKCLMRLKP TLHGPTPLLY 1022

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggylaalaaYCLSTGCVVIVGRV 660
 RLGAVQNE+TLTHP+TKYI+TCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+
 Sbjct 1023 RLGAVQNEVTLTHPITKYIITCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1082

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 +LSGKPA+IPDREVLRY+ FDEMEEC
 Sbjct 1083 ILSGKPAVIPDREVLRYQAFDEMEEC 1107

> gi|2943784|dbj|BAA25076.1| polyprotein [Hepatitis C virus]

Length=3010

Score = 1207 bits (3123), Expect = 0.0, Method: Composition-based stats.
Identities = 619/685 (90%), Positives = 658/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NG CWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLSLTGRDKNQVEGEVQVVSTAKQSFLATCVNGACWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSSTPCTCGSSDLVLRHADVIPVrrrg	120
		++T+A+ KGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLVLRHADVIPVRRRG	
Sbjct	1087	SKTLAAAKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLVLRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCP+GH VGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGY VLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYMVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAET GAR VVLATATPPGS+T PHPNIEEV L+ TGEIPFY K IP+EVI+	
Sbjct	1327	LGIGTVLDQAETVGARFVVLATATPPGSITFPHPNIEEVPLANTGEIPFYAKTIPIEVIR	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALPAKLSALGLNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRTQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEVFTGLT	540
		RPS MFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSAMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARA+APPPSWDMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAKAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYQEFDEMEEC 1711	

> [gi|81960062|sp|Q913D4|POLG_HCVIN](#) Genome polyprotein [Contains: Core protein p21 (C; C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]

gi|15422183|gb|AAK95832.1| polyprotein [Hepatitis C virus (isolate India)]
Length=3011

Score = 1207 bits (3123), Expect = 0.0, Method: Composition-based stats.
Identities = 623/685 (90%), Positives = 651/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCI+TSLTGRDKNQVEGE+QIVSTA QTFLATCING CWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIVTSLTGRDKNQVEGEIQIVSTATQTFLATCINGACWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		+RTIAS GPV++MYTNVDQDLVGWPAPQG+RSLTPCTCG+SDLYLVRHADVIPVRRRG	
Sbjct	1087	SRTIASASGPVVRMYTNVDQDLVGWPAPQGARSLTPCTCGASDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCAPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRPISYLGSSGGPLLC GH GIFRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1147	DNRGSLLSPRPISYLGSSGGPLLCPMGHVAGIFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFTDNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPTVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTTGSPITYSTYKGFLADGGC GGAYDIIICDECHS DATSI	
Sbjct	1267	YMSKAHGIDPNVRTGVRTITTTGSPITYSTYKGFLADGGCPGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RL VLATATPPG VTVPH NIEEVALS GE PFYGKAIP L IK	
Sbjct	1327	LGIGTVLDQAETAGVRLTVLATATPPGLVTVPHSNIEEVALSADGEKPFYGKAIP LNYIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLV ALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AAKLV LG+NAVA+YRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELA AAKLVGLGVNAVAFYRGLDVSVIPPTTGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCV QTVD FSLD F+IET T+PQDAVSR+QRRGRTGRGK GIYR+V+PGE	
Sbjct	1447	DFDSVIDCNTCVVQTVD FSLDPIFSIETSTVPQDAVSRSQRRGRTGRGKHGIYRYVSPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDS VLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSVVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARA+APPPSWDQMWKCLIRLKP TL G TPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARARAPPPSWDQMWKCLIRLKP TLTGATPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
		RLG+VQNEITLTHP+T+YIM CMSADLEVVTSTWVLVGGVLAALAAAYCLSTG VVIVGR+	
Sbjct	1627	RLGSVQNEITLTHPITQYIMCMSADLEVVTSTWVLVGGVLAALAAAYCLSTGSSVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+L GKPA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILGGKPAVIPDREVLYREFDEMEEC 1711	

> gi|38492205|gb|AAR22408.1| polyprotein [Hepatitis C virus]
Length=3011

Score = 1204 bits (3114), Expect = 0.0, Method: Composition-based stats.
Identities = 616/685 (89%), Positives = 653/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRP+SYLKGS SGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP V PQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHG +PNIRTGVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQA+T GARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIET T+P RGRTRGRG+ G YRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLGAVQNE++LTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	LSG+PA+IPDREVLY+EFDEMEEC	1711

> gi|306287|gb|AAA45721.1| putative
Length=3010

Score = 1199 bits (3102), Expect = 0.0, Method: Composition-based stats.
Identities = 619/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	

Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgslspsrPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLL PRP+SYLKSSGGPLLCP+GHAVGI AAVCTRGVA AV+FIPVE++ETTM	
Sbjct	1147	DGRGSLPPRPVSYLKSSGGPLLCPSGHAVGILPAAVCTRGVAMAVEFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDN SPP VPQ+FQVAHLHAPTGS GKST+VPAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNPSPPAVPQTFQVAHLHAPTGS GKSTRVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTTG+PITYSTYKFLADGG SGGAYDII+CDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNLRTGVRTITTTGAPITYSTYKFLADGGSGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHNIEEVALSTTGEIPFYGKAIPLEVIK	360
		GIGTVLDQAETAGARLVVL+TATPPGSVTVPH NIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	YGIGTVLDQAETAGARLVVLSTATPPGSVTVPHLNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTTET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTTETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEF EGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFSEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVA YQATVCARAQAPPPSWD+MW+CLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVA YQATVCARAQAPPPSWDEMWRLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCSADLEVVTSTWVlvvggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IMTCSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFIMTCSADLEVVTSTWVVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQEFDEMEEC 1711	

> gi|50235322|gb|AAT69968.1| polyprotein [Hepatitis C virus]
 Length=3011

Score = 1199 bits (3101), Expect = 0.0, Method: Composition-based stats.
 Identities = 626/685 (91%), Positives = 648/685 (94%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVI MYTNVDQDL GW APQ SLTP +CGSSDLYLVTRHADVIPV RRG	
Sbjct	1087	TRTIASSKGPVILMYTNVDQDLGGWTAPQVLGSLTPWSCGSSDLYLVTRHADVIPVPRRG	1146
Query	121	dsrgslspsrPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		++RGSLLSPRPISYLKSSGGPLLCP GHAVGIFRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1147	ETRGSLSPRPISYLKSSGGPLLCPMGHAVGIFRAAVCTRGVAKAVDFVPVESLETTMR	1206

Query	181	SPVF T DNSSPPVVPQSFQVAHLHAPTGS G SKTKVPAA Y AAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVF T DNSSP VPQS+QVAHLHAPTGS G SKTKVPAA Y AAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY G KFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY G KFLADGGC GGAYDIIICDECHS DATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAG RL VLATATPPGSVTVPH NIEEVALS GEIPFYGKAIP L IK	1386
Query	361	GGRHLIFCHSKKKKCELA A AKLV A GINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA A AKLVGPGVNAVAFYRGLDVSVIPPTGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD F SLDPTFTTITETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCV QTVD F SLDP F+IET T+PQDAVSR+QRRGRTGRGK GIYR+V+PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDS VLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL V AYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGEN PYL V AYQATVCARA+APPPSWDQMWKCLIRLKPTL G TPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMT C SADLEVVTSTWv l vggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLG+VQNEITLTHP+T+YIM C SADLEVVTSTWVLVGGVLAALAAAYCLSTG VVIVGR+	1686
Query	661	VL S GKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	+L GKPA+IPDREVLYREFDEMEEC 1711	

> [gi|567060|gb|AAA52748.1|](#) polyprotein
Length=3010

Score = 1198 bits (3100), Expect = 0.0, Method: Composition-based stats.
Identities = 619/685 (90%), Positives = 659/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYL V TRHADVIPVrrrg	120
Sbjct	1087	++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYL V TRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLL PRP+SYLKSSGGPLLCP+GHAVGI AAVCTRGVA AV+FIPVE++ETTMR	1206
Query	181	SPVF T DNSSPPVVPQSFQVAHLHAPTGS G SKTKVPAA Y AAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVF T DN SPP VPQ+FQVAHLHAPTGS G SKT+VPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY G KFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTG+PITYSTY G KFLADGG SGGAYDII+CDECHSTD+T+I	

Sbjct	1267	YMSKAHGIDPNLRTGVRTITTTGAPITYSTYGKFLADGGGSGGAYDIIMCDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		GIGTVLDQAETAGARLVVL+TATPPGSVTVPH NIEEVALS TGEIPFYGKAIP+E IK	
Sbjct	1327	YGIGTVLDQAETAGARLVVLSTATPPGSVTVPHLNIEEVALSNTGEIPFYGKAIPIEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKSLGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRAGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTIVRLRAYMNTPLPVCQDHLFEWGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPLPVCQDHLFE EGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPLPVCQDHLFESEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+GEN PYLVAQATVCARAQAPPPSWD+MW+CLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGENFPYLVAQATVCARAQAPPPSWDEMWRCCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHP+TK+IMTCMSADLEVVTSTWVVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTLTHPITKFINTCMSADLEVVTSTWVVLVGGVLAALAAAYCLTTGGSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSGKPAIIPDREVLY+EFDEMEEC	
Sbjct	1687	ILSGKPAIIPDREVLYQEFDEMEEC 1711	

>gi|5748511|emb|CAB53095.1| polyprotein [Hepatitis C virus type 1b]
Length=3010

Score = 1197 bits (3098), Expect = 0.0, Method: Composition-based stats.
Identities = 627/685 (91%), Positives = 663/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		A ITAY+QQTRGLLGCIITSLTGRD+NQVEGEVQ+VSTA Q+FLATC+NGVCWTVYHGAG	
Sbjct	1027	AHITAYSQQTRGLLGCIITSLTGRDRNQVEGEVQMVSTATQSFLATCVNGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRP+SYLKSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DSRGSLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATL FGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSCGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRT TTTG+PITYSTYGKFLADGGCSCGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGIDPNIRTGVRTTTTGTGAPITYSTYGKFLADGGCSCGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS+TGE+PFYGKAIP+E IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSSTGEVPFYGKAIPETIK	1386

Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL LG+NAVAYYRGLDVSVIP GDV+VVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKSLGLLNAVAYYRGLDVSVIPTSGDVIVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRIGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLWAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlgvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+T THP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEVTTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLRYREFDEMEEC	685
		VLSGKPAIIPDREVLRYREFDEMEEC	
Sbjct	1687	VLSGKPAIIPDREVLRYREFDEMEEC	1711

> gi|437108|gb|AAA75355.1| polyprotein
Length=3010

Score = 1197 bits (3098), Expect = 0.0, Method: Composition-based stats.
Identities = 621/685 (90%), Positives = 652/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGW A G RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWQAAPGMRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRP+SYLGSSGGPLL P+GHAVGIFRAAVCTRGVAKAVDF+PVE++ETTMR	
Sbjct	1147	DGRGSLLSPRPVSYLGSSGGPLLWPSPGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQTFQVAHLHAPTSGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG RTITTG+PITYSTYGKF ADGGCGSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGARTITTGAPITYSTYGKFFADGGCGSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLD+AETAGARLVVLATATPPGS TVPHPNIEEVAL TGEIPFYG+AIP+E IK	
Sbjct	1327	LGIGTVLDRAETAGARLVVLATATPPGSTTVPHPNIEEVALPNTGEIPFYGRAPIEFIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFC SKKKKCELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCPSKKKKCELAALKLSALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET T+PQDAVSRTQRRGRTGRG+ GIYRFV PGE	

Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRTQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWE VFTGL	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPLPVCQDHLEFWESVFTGLN	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQAPPPSWDQMWKCLI LKP LHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQAPPPSWDQMWKCLIWLKPV LHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvvgvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TK IM MSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKLIMASMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		+LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC 1711	

> [gi|7650258|gb|AAF65960.1|](#) polyprotein [Hepatitis C virus]
 Length=3010

Score = 1195 bits (3092), Expect = 0.0, Method: Composition-based stats.
 Identities = 624/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATCING CWTVYHGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCINGACWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ Q+YTNVDQDL+GW AP GRSRS LTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQIYTNVDQDLLGWQAPPGSRS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RGSLLSPRP+SYLKSSGGP L LCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DTRGSLLSPRPVSYLKSSGGP L LCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQT FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG RTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T++	
Sbjct	1267	YMSKAHGTDPNIRTGTRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTV	1326
Query	301	LGIGTVLDQAETAGARLVV LATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVV LATATPPGSVTVPH NIEEVAL+ TGEIPFYGKAIP++VIK	
Sbjct	1327	LGIGTVLDQAETAGARLVV LATATPPGSVTVPHSNIEEVALTNTGEIPFYGKAIPIDVIK	1386
Query	361	GGRHLIFCHSKKKKDELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA AAKL ALG+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELA AAKLSALGLNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDS IDCNTCVTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSXIDCNTCVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRGGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETS VRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLG VQNE+TLTHP+TK+IM CMSADLEVVTSTWVlvvggvlaalaaYCL+TG VVIVGR+	
Sbjct	1627	RLGPVQNEVTLTHPITKFIMACMSADLEVVTSTWVlvvggvlaalaaYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PA+IPDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPAVIPDREVLYREFDEMEEC	1711

>gi|4753721|emb|CAB41951.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1193 bits (3086), Expect = 0.0, Method: Composition-based stats.
Identities = 625/685 (91%), Positives = 662/685 (96%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ+VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVFHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGP+ QMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLV+RHADVIPVRRRG	
Sbjct	1087	SKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVSRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRP+SYLKSSGGPLLCP+GH GIFRAAVCTRGVAKAVDF+PVE++ETT R	
Sbjct	1147	DSRGSLLSPRPVSYLKSSGGPLLCPSGHVAGIFRAAVCTRGVAKAVDFVPVESMETTTR	1206
Query	181	SPVFETDNSSPPVVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFETDNSSPP VPQ+FQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATL FGA	
Sbjct	1207	SPVFETDNSSPPAVPQTFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVLNPSVAATLSFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DP+IRTG RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+TSI	
Sbjct	1267	YMSKAHGVDPSIRTGTRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGEIPFYGKAIP+E I+	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIR	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GG HLIFCHSKKKCDELAAL+L +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGGHLIFCHSKKKCDELAALSSLGVNAVAYYRGLDVSVIP TSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITLPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTTET T+PQDAVSR+QRRGRTGRGK GIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETTTVPQDAVSRQRRGRTGRGKRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAET+VRLRAY+NT PGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETSRLRAYLNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNE+TLTHPVTKYIM CMSADLEVVTSTWVlvvggvlaalaaYCL+TG VVIVGR+	

Sbjct 1627 RLGAVQNEVTLTHPVTKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
+LSGKPAIIPDREVLRYREFDEMEEC

Sbjct 1687 ILSGKPAIIPDREVLRYREFDEMEEC 1711

> gi|7650262|gb|AAF65962.1| polyprotein [Hepatitis C virus]
Length=3010

Score = 1193 bits (3086), Expect = 0.0, Method: Composition-based stats.
Identities = 626/685 (91%), Positives = 665/685 (97%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQ+VSTA Q+FLATCINGVCWTV+HGAG

Sbjct 1027 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQVSTATQSFLATCINGVCWTVFHHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg 120
++T+A PKGP+ QMYTNVDQDLVGW AP G+RSLTPCTCGSSDLVLRHADVIPVRRRG

Sbjct 1087 SKTLAGPKGPITQMYTNVDQDLVGWLAPPGARSLTPCTCGSSDLVLRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLKGS SGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
DSRGSLLSPRPISYLKGS SGGPLLCP+GH VG+FRAAVCTRGVAKAVDFIPVE++ETTMR

Sbjct 1147 DSRGSLLSPRPISYLKGS SGGPLLCPSGHVVLFRFAAVCTRGVAKAVDFIPVEHMETTMR 1206

Query 181 SPVFETDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA 240
SPVFETDNSSPP VPQ+FQVAHLHAPTGS GKST+VPAAYAAQGYKVLVNLPSVAATL FGA

Sbjct 1207 SPVFETDNSSPPAVPQAFQVAHLHAPTGS GKSTRVPAAYAAQGYKVLVNLPSVAATLSFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI 300
YMSKA+G+DPNIRTG RTITTG+ ITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I

Sbjct 1267 YMSKAYGVDPNIRTGTRTITTGASITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
LGIGTVLDQAETAGARLVVLATATPPGSVTVPHP+IEEVALS TGEIPFYGKAIP+EVIK

Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPSIEEVALSNTGEIPFYGKAIPIEVIK 1386

Query 361 GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
GGRHLIFCHSKKKKCELA AAKL +LG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG

Sbjct 1387 GGRHLIFCHSKKKKCELA AAKLSSLGMNAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG 1446

Query 421 DFDSVIDCNCVQTQTVDFSLDPTFTTITITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE 480
DFDSVIDCNCVQTQTVDFSLDPTFTT+T T+PQDAVSR+QRRGRTGRG+PGIYRFV PGE

Sbjct 1447 DFDSVIDCNCVQTQTVDFSLDPTFTTIDTTTVPQDAVSRSQRRGRTGRGRPGIYRFVTPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
RPSGMFDSSVLCECYDAGCAWYEL PAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT

Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELAPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
HIDAHFLSQTKQ+G+N PYLVA YQATVCARAQA PPSWDQMWKCLIRLKP TLHGPTPLLY

Sbjct 1567 HIDAHFLSQTKQAGDNFPYLVA YQATVCARAQALPPSWDQMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV 660
RLGAVQNE+TLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+

Sbjct 1627 RLGAVQNEVTLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI 1686

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
+LSG+PA++PDREVLRYREFDEMEEC

Sbjct 1687 ILSGRPAVVPDREVLRYREFDEMEEC 1711

> gi|1405417|dbj|BAA09919.1| E1 and E2/NS1 envelope glycoprotein [Hepatitis C virus]
Length=3010

Score = 1191 bits (3080), Expect = 0.0, Method: Composition-based stats.
Identities = 614/685 (89%), Positives = 653/685 (95%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAY+QQTRGLLGCIITSLTGRDKNQVEGEVQ VSTA Q+FLATC+NGVCWTV+HGAG	
Sbjct	1027	APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQEVSTATQSFLATCVNGVCWTVFHHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLVTRHADVIPVrrrg	120
		++ + PKGP+ QMYT+VDQDLVGW G+RSLTP TCGSS LYLVTR+ADVIPVRR G	
Sbjct	1087	SKILVGPKGPITQMYTSVDQDLVGWVERPGARSLTPGTCGSSVLVLVTRNADVIPVRRGG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSP+P+SYLGSSGGPLLCP+GHAVGIFRAAVCTRGVAKAVDFIPVE++ETTMR	
Sbjct	1147	DGRGSLLSPKPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVESMETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		S VFTDNSSPP VPQ+FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SLVFTDNSSPPAVPQAFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG DPNIRTG+RTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAHGTDPNIRTGIRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALS TGE+PFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSNTGEVPPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL LGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLSTLGINAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYRFV PGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTVPQDAVSRQRRGRTGRGRRGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWGVFTGLT	540
		RP GMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPG VCQD+LEFWE VFTGLT	
Sbjct	1507	RPLGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNTPGFAVCQDYLEFWEDVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HI++HFLSQTKQ+G+N PYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIESHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCL+TG VVIVGR+	
Sbjct	1627	RLGAVQNEITLTHPITKYIMTCMSADLEVVTSTWVLVGGVLAALAAAYCLTTGSSVVIVGRI	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		+LSG+PA++PDREVLYREFDEMEEC	
Sbjct	1687	ILSGRPVAVPDREVLYREFDEMEEC	1711

> gi|67810846|gb|AA82011.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1174 bits (3037), Expect = 0.0, Method: Composition-based stats.
Identities = 606/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	1446
Query	421	DFDSVIDCNCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVT KY 618	
Sbjct	1627	RLGAVQNE+TLTHP+TKY 1644	

> gi|67810857|gb|AA Y82016.1| polyprotein [Hepatitis C virus]
Length=1646

Score = 1172 bits (3033), Expect = 0.0, Method: Composition-based stats.
Identities = 607/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1029	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWP PQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180

Sbjct	1149	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1209	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1269	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	360
Sbjct	1329	LGIGTVLDQAESAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1389	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1449	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY	600
Sbjct	1569	HIDAHFLSQTKQSGENFPYL VAYQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+TLTHPVTKY	
Sbjct	1629	RLGAVQNEVTLTHPVTKY 1646	

>gi|67810849|gb|AA Y82012.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1172 bits (3032), Expect = 0.0, Method: Composition-based stats.
Identities = 605/618 (97%), Positives = 612/618 (99%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1147	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMS+AHG+DPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSRAHGVDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1326

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLAALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET TLPQ+AVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTLPQEAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTIVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTIVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTIVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHPVTKY	
Sbjct	1627	RLGAVQNEVTLTHPVTKY 1644	

> gi|67810875|gb|AA82024.1| polyprotein [Hepatitis C virus]
gi|67810873|gb|AA82023.1| polyprotein [Hepatitis C virus]
 Length=1646

Score = 1171 bits (3030), Expect = 0.0, Method: Composition-based stats.
 Identities = 607/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1029	APITAYAQQTRGLLGCIITSLSLGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1149	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1209	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGFADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPN+RTGVRTITTGSPITYSTYGFADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1269	YMSKAHGIDPNLRTGVRTITTGSPITYSTYGFADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1329	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1389	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1448

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1449	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYE TPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYEPTAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1569	HIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHPVTKY	
Sbjct	1629	RLGAVQNEVTLTHPVTKY 1646	

> [gi|67810866|gb|AA82020.1|](#) polyprotein [Hepatitis C virus]
Length=1646

Score = 1171 bits (3029), Expect = 0.0, Method: Composition-based stats.
Identities = 607/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1029	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPAPQARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1149	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1209	SPVFTDNSSPPAVVPQSFQVAHLHAPTGSGBKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDEC STDATSI	
Sbjct	1269	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECRSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1329	LGIGTVLDQAESAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1389	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1449	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	

Sbjct 1569 HIDAFLSQTQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 1628

Query 601 RLGAVQNEITLTHPVTKY 618
 RLGAVQNE+TLTHPVTKY

Sbjct 1629 RLGAVQNEVTLTHPVTKY 1646

> [gi|67810879|gb|AA82026.1|](#) polyprotein [Hepatitis C virus]
 Length=1644

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.
 Identities = 606/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG

Sbjct 1027 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 1086

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 TRTIASPKGPVIQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG

Sbjct 1087 TRTIASPKGPVIQMYTNVDQDLVGWPAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1146

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR

Sbjct 1147 DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR 1206

Query 181 SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA

Sbjct 1207 SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 1266

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI

Sbjct 1267 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 1326

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEE ALSTTGEIPFYGKAIPLE IK

Sbjct 1327 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEALSTTGEIPFYGKAIPLEAIK 1386

Query 361 GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKCELAALKLVA+GINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG

Sbjct 1387 GGRHLIFCHSKKKKCELAALKLVAMGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG 1446

Query 421 DFDSVIDCNCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgqKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE

Sbjct 1447 DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE 1506

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT

Sbjct 1507 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 1566

Query 541 HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY

Sbjct 1567 HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 1626

Query 601 RLGAVQNEITLTHPVTKY 618
 RLGAVQNE+TLTHP+TKY

Sbjct 1627 RLGAVQNEVTLTHPITKY 1644

> [gi|67810877|gb|AA82025.1|](#) polyprotein [Hepatitis C virus]
 Length=1644

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.
Identities = 606/618 (98%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIIT LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	1206
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPP VPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLV+GINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPQDAVSrtqrrgrtgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1627	RLGAVQNE+TLTHP+TKY 1644	

> [gi|67810842|gb|AAY82009.1|](#) polyprotein [Hepatitis C virus]
Length=1644

Score = 1170 bits (3027), Expect = 0.0, Method: Composition-based stats.
Identities = 605/618 (97%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGS DLYLVTRHADVIPVRRRG	1146

Query	121	dsrgsllsprPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDII+VCDCHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHP+TKY	
Sbjct	1627	RLGAVQNEVTLTHPITKY 1644	

> [gi|67810859|gb|AA82017.1|](#) polyprotein [Hepatitis C virus]
 Length=1646

Score = 1170 bits (3026), Expect = 0.0, Method: Composition-based stats.
 Identities = 606/618 (98%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1029	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWP PQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1149	DSRGSLSPRPISYLGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1209	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300

Sbjct	1269	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1329	LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1388
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1389	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
Sbjct	1449	DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1569	HIDAHFLSQTKQSGENFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1629	RLGAVQNE+TLTHPVTKY 1646	

> gi|67810855|gb|AA82015.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1169 bits (3023), Expect = 0.0, Method: Composition-based stats.
Identities = 604/618 (97%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D RGSLLSPRPISYLGSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP V P Q S F Q V A H L H A P T G S G K S T K V P A A Y A A Q G Y K V L V L N P S V A A T L G F G A	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSRAHGVDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKL A L G I N A V A Y Y R G L D V S V I P G D V V V V A T D A L M T G + T G	1446

Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHPVTKY	
Sbjct	1627	RLGAVQNEVTLTHPVTKY 1644	

>gi|67810853|gb|AA82014.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1169 bits (3023), Expect = 0.0, Method: Composition-based stats.
Identities = 604/618 (97%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSITGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSITGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSITGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSITPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASSKGPVIQMYTNVDQDLVGWPAPQARSITPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMS+AHG+DPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSRAHGVDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALK ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKCDELAALKLAALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600

Sbjct 1567 HIDAHFSLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1626
 Query 601 RLGAVQNEITLTHPVTKY 618
 RLGAVQNE+TLTHPVTKY
 Sbjct 1627 RLGAVQNEVTLTHPVTKY 1644

> gi|67810868|gb|AA82021.1| polyprotein [Hepatitis C virus]
 Length=1646

Score = 1168 bits (3021), Expect = 0.0, Method: Composition-based stats.
 Identities = 606/618 (98%), Positives = 610/618 (98%), Gaps = 0/618 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
 Sbjct 1029 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 1088

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 1089 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 1148

Query 121 dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR
 Sbjct 1149 DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR 1208

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVFTDNSSPP VPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
 Sbjct 1209 SPVFTDNSSPPAVPQSFQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 1268

Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI 300
 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI
 Sbjct 1269 YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCGSGGAYDIIICDECHSTDATSI 1328

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
 Sbjct 1329 LGIGTVLDQAESAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 1388

Query 361 GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIP GDVVVVATDAL TGYTG 420
 GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIP GDVVVVATDAL TGYTG
 Sbjct 1389 GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPTSGDVVVVVATDALTTGYTG 1448

Query 421 DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE 480
 DFDSVIDCNCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE
 Sbjct 1449 DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE 1508

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFW GVFTGLT
 Sbjct 1509 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWGVFTGLT 1568

Query 541 HIDAHFSLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
 HIDAHFSLSQTKQSGEN PVLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
 Sbjct 1569 HIDAHFSLSQTKQSGENFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 1628

Query 601 RLGAVQNEITLTHPVTKY 618
 RLGAVQNE+TLTHPVTKY
 Sbjct 1629 RLGAVQNEVTLTHPVTKY 1646

> gi|67810883|gb|AA82028.1| polyprotein [Hepatitis C virus]
 Length=1644

Score = 1167 bits (3020), Expect = 0.0, Method: Composition-based stats.
Identities = 605/618 (97%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAP G+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSSPP VPPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1386
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKCDELAACKLVA+G+NAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQA PPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1627	RLGAVQNE+TLTHP+TKY	
		RLGAVQNEVTLTHPITKY 1644	

>[gi|28921568|ref|NP_803144.1| G NS3 protease/helicase' [Hepatitis C virus]
Length=631

Score = 1167 bits (3019), Expect = 0.0, Method: Composition-based stats.
Identities = 618/631 (97%), Positives = 624/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTA QTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	

Sbjct	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSALTPTCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCAGHAVG+FRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	121	DSRGSLLSPRPISYLGSSGGPLLCAGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMR	180
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHG+DPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGVDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Query	361	GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIP GDVVVV+TDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIP TSGDVVVVSTDALMTGFTG	420
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	421	DFDSVIDCNCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEVTLTHPITKYIMTCMSADLEVVT 631	

>gi|67810881|gb|AAY82027.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1167 bits (3019), Expect = 0.0, Method: Composition-based stats.
Identities = 605/618 (97%), Positives = 611/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAA+TFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAARTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSALTPTCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAP G+RSLTPTCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPPGARSALTPTCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLVAMGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQA PPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1627	RLGAVQNE+TLTHP+TKY	
		RLGAVQNEVTLTHPITKY 1644	

> [gi|67810887|gb|AA82030.1|](#) polyprotein [Hepatitis C virus]
 Length=1644

Score = 1167 bits (3018), Expect = 0.0, Method: Composition-based stats.
 Identities = 602/618 (97%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEV IVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSR SLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFETDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFETDNSSPP VPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGS IYTYSTYKGFLADGGCSGGAYDIIICDECHS DATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA+KLVALGINAVAYYRG+DVSVIP GDVVVVATDALMTGYTG	

Sbjct	1387	GGRHLIFCHSKKKKDELASKLVALGINAVAYYRGIDVSVIPTSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTQKQSGEN PYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TL GPTPLLY	
Sbjct	1567	HIDAHFLSQTQKQSGENFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

>gi|67810844|gb|AA Y82010.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1166 bits (3016), Expect = 0.0, Method: Composition-based stats.
Identities = 602/618 (97%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRG LLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRG LLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRG LLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RS LTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISY LKSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISY LKSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLSPRPISY LKSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTIT TGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTIT TGSPITYSTY GKFLADGGCSGGAYDII+CDECHSTDATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTIT TGSPITYSTY GKFLADGGCSGGAYDIIVCDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTV D E AGARLVVLATATPPGSVTV HPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1327	LGIGTVFDPPENAGARLVVLATATPPGSVTVSHPNIEEVALSTTGEIPFYGKAIPLEAIK	1386
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIP IG DVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1566

Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY	618
		RLGAVQNE+TLTHP+TKY	
Sbjct	1627	RLGAVQNEVTLTHPVTKY	1644

> gi|67810870|gb|AA82022.1| polyprotein [Hepatitis C virus]
Length=1646

Score = 1165 bits (3013), Expect = 0.0, Method: Composition-based stats.
Identities = 604/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1029	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1149	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1209	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSCGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSCGGAYDIIICDECHSTDATSI	
Sbjct	1269	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSCGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	1329	LGIGTVLDQAESAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	
Sbjct	1389	GGRHLIFCHSKKKCDELAALKLVALGINAVAYYRGLDVSVIP TSGDVVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgkPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET QDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1449	DFDSVIDCNTCVTQTVDFSLDPTFTIETTNASQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PVLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	
Sbjct	1569	HIDAHFLSQTKQSGENFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY	618
		RLGAVQN +TLTHPVTKY	
Sbjct	1629	RLGAVQNGVTLTHPVTKY	1646

> gi|67810851|gb|AA82013.1| polyprotein [Hepatitis C virus]

Length=1644

Score = 1165 bits (3013), Expect = 0.0, Method: Composition-based stats.
Identities = 603/618 (97%), Positives = 609/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	1147	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1206
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSKTKVPAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMS+AHG+DPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	1267	YMSRAHGVDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETA ARLVVLATATPPGSVTVPHPNIEEVA STTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAWARLVVLATATPPGSVTVPHPNIEEVAPSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAALKL ALGINAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELAALKLAALGINAVAYYRGLDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDLSLDPFTTETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDLSLDPFTTET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDLSLDPFTTETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPT LLY	
Sbjct	1567	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTLLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+TLTHPVTKY	
Sbjct	1627	RLGAVQNEVTLTHPVTKY 1644	

> gi|67810896|gb|AA82034.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1164 bits (3010), Expect = 0.0, Method: Composition-based stats.
Identities = 602/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120

Sbjct	1087	TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG TRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLKGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLKGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFNDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFNDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFNDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGS ITYSTYKGFLADGGCSGGAYDIIICDECHS DATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSSITYSTYKGFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA+KLVLGINAVAYYRG+DVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAASKLVTLGINAVAYYRGIDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgjrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> gi|67810861|gb|AA82018.1| polyprotein [Hepatitis C virus]
Length=1646

Score = 1163 bits (3009), Expect = 0.0, Method: Composition-based stats.
Identities = 604/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1029	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWP PQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPTPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLKGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLKGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1149	DSRGSLSPRPISYLKGSSGGPLPCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFNDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFNDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1209	SPVFNDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1268

Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1269	YMSKA GIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1329	LGIGTVLDQAE+AGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	1388
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP GDVVVVATDALMTGYTG	420
Sbjct	1389	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIP TSGDVVVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1449	DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDS SVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1509	RPSGMFDS VLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1568
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1569	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	1628
Query	601	RLGAVQNEITLTHPVTKY 618	
Sbjct	1629	RLGAVQNE+T THPVTKY 1646	

> gi|67810894|gb|AAV82033.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1162 bits (3007), Expect = 0.0, Method: Composition-based stats.
Identities = 601/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVF TDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVF TDNSSPP VPPQSFQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGS ITYSTYGKFLADGGCSGGAYDIIICDECHS DATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420

Sbjct	1387	GGRHLIFCHSK+KCDELA+KLV LGINAVAYYRG+DVSVIP GDV VVVATDALMTG+TG GGRHLIFCHSKRKDELAASKLVTLGINAVAYYRGIDVSVIPTSGDV VVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> [gi|67810864|gb|AAY82019.1|](#) polyprotein [Hepatitis C virus]
Length=1646

Score = 1162 bits (3007), Expect = 0.0, Method: Composition-based stats.
Identities = 603/618 (97%), Positives = 608/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1029	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1088
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRS LTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1089	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGARS LTPCTCGSSDLYLVTRHADVIPVRRRG	1148
Query	121	dsrgsllsprPISYLGSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLLSPRPISYLGSSGGP L C AGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	180
Sbjct	1149	DSRGSLLSPRPISYLGSSGGP LCLAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	1208
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ FQVAHLHAPTG+GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1209	SPVFTDNSSPPAVPQCFQVAHLHAPTGN GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1268
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1269	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	1328
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAE+AGARLVVLATATPPGSVTVPH NIEEVALSTTGEIPFYGKAIPLE IK	360
Sbjct	1329	LGIGTVLDQAESAGARLVVLATATPPGSVTVPHSNIEEVALSTTGEIPFYGKAIPLEAIK	1388
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFC SKKKKDELA AKLVALGINAVAYYRGLDVSVIP GDV VVVATDALMTGYTG	420
Sbjct	1389	GGRHLIFCRSKKKKDELA AKLVALGINAVAYYRGLDVSVIP TSGDV VVVATDALMTGYTG	1448
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1449	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1508
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1509	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1568

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Query   541   HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY   600
          HIDAHFLSQTKQSGEN PYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   1569   HIDAHFLSQTKQSGENFPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY   1628

Query   601   RLGAVQNEITLTHPVTKY   618
          RLGAVQNE+TLTHPVTKY
Sbjct   1629   RLGAVQNEVTLTHPVTKY   1646

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> gi|68012750|gb|AAV84771.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1161 bits (3004), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 622/631 (98%), Gaps = 0/631 (0%)

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Query    1   APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG   60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct    1   APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG   60

Query   61   TRTIASPKGPVIQMYTNVDQDLVGWPAQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg   120
          T+TIAS KGPVIQMYTNVDQDLVGWPAQGS+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct   61   TKTIASSKGPVIQMYTNVDQDLVGWPAQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG   120

Query   121   dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR   180
          DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct   121   DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR   180

Query   181   SPVFSDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA   240
          SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct   181   SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA   240

Query   241   YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI   300
          YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI
Sbjct   241   YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI   300

Query   301   LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK   360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct   301   LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK   360

Query   361   GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG   420
          GGRHLIFCHSKKKKCELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct   361   GGRHLIFCHSKKKKCELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG   420

Query   421   DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE   480
          DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRG+TGRGKPGIYRFV PGE
Sbjct   421   DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGKTGRGKPGIYRFVTPGE   480

Query   481   RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT   540
          RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Sbjct   481   RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT   540

Query   541   HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY   600
          HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   541   HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY   600

Query   601   RLGAVQNEITLTHPVTKYIMTCMSADLEVVT   631
          RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct   601   RLGAVQNEITLTHPITKYIMTCMSADLEVVT   631

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> gi|68012736|gb|AA84764.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012730|gb|AA84761.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012720|gb|AA84756.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012702|gb|AA84747.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1161 bits (3004), Expect = 0.0, Method: Composition-based stats.
Identities = 615/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	61	TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	180
Query	181	SPVFETDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	360
Query	361	GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKKCELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
Sbjct	601	RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	631

> gi|67810898|gb|AA82035.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1161 bits (3003), Expect = 0.0, Method: Composition-based stats.
Identities = 601/618 (97%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
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Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA PVFTDNSSPP VPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	PPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTGS ITYSTYGKFLADGGCSGGAYDIIICDECHS DATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSSITYSTYGKFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLV ALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA+KLV LGINAVAYYRG+DVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKCDELA SKLVTLGINAVAYYRGIDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> [gi|67810892|gb|AAY82032.1|](#) polyprotein [Hepatitis C virus]
Length=1644

Score = 1161 bits (3003), Expect = 0.0, Method: Composition-based stats.
Identities = 600/618 (97%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Sbjct	1087	TRTIASPKGPVIQMYTNVDKDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGS ITYSTYKGFLADGGCSGGAYDIIICDECHS DATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTTGSSITYSTYKGFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCEDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSK+KCEDELA+KLV LGINAVAYYRG+DVSVIP GDVVVVATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKRKCEDELAASKLVTLGINAVAYYRGIDVSVIPTSGDVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNCVTQTVDVDFSLDPTFTTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
		DFDSVIDCNCVTQTVDVDFSLDPTFTTIET TLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	
Sbjct	1447	DFDSVIDCNCVTQTVDVDFSLDPTFTTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618	
		RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> [gi|68012718|gb|AA84755.1|](#) nonstructural protein 3 [Hepatitis C virus]
[gi|68012716|gb|AA84754.1|](#) nonstructural protein 3 [Hepatitis C virus]
[gi|68012700|gb|AA84746.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1161 bits (3003), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300

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Query   301  LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK  360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct   301  LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK  360

Query   361  GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG  420
          GGRHLIFCHSKKKKCELAALKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct   361  GGRHLIFCHSKKKKCELAALKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG  420

Query   421  DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE  480
          DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE
Sbjct   421  DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE  480

Query   481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT  540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT
Sbjct   481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEGVFTGLT  540

Query   541  HIDAHFSLQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600
          HIDAHFSLQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct   541  HIDAHFSLQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600

Query   601  RLGAVQNEITLTHPVTKYIMTCMSADLEVVT  631
          RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct   601  RLGAVQNEITLTHPITKYIMTCMSADLEVVT  631

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> [gi|68012706|gb|AAV84749.1|](#) nonstructural protein 3 [Hepatitis C virus]
[gi|68012704|gb|AAV84748.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1160 bits (3001), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

```

Query    1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG  60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct    1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG  60

Query    61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg  120
          TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct    61  TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG  120

Query   121  dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR  180
          D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct   121  DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR  180

Query   181  SPVFTDNSSPPVVPQS+QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA  240
          SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct   181  SPVFSDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA  240

Query   241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI  300
          YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI
Sbjct   241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI  300

Query   301  LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK  360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct   301  LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK  360

Query   361  GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG  420
          GGRHLIFCHSKKKKCELAALKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct   361  GGRHLIFCHSKKKKCELAALKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG  420

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Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNE+TLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEVTLTHPITKYIMTCMSADLEVVT 631	

> [gi|68012748|gb|AAY84770.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.
Identities = 615/631 (97%), Positives = 623/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE+LETTMR	
Sbjct	121	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVESLETTMR	180
Query	181	SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELA AKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	

Sbjct 541 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
 RLGAVQNEITLTHP+TKYIMTCMSADLEVVT

Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

> gi|68012732|gb|AAI84762.1| nonstructural protein 3 [Hepatitis C virus]
 Length=631

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.
 Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG

Sbjct 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg 120
 T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG

Sbjct 61 TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG 120

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR

Sbjct 121 DDRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR 180

Query 181 SPVFTDNSSPPVVPQS FQVAHLHAPT GSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVF+DNSSPP VPQS+QVAHLHAPT GSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA

Sbjct 181 SPVFSDNSSPPAVPQSYQVAHLHAPT GSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI

Sbjct 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK

Sbjct 301 LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 360

Query 361 GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG 420
 GGRHLIFCHSKKKCDELA AKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG

Sbjct 361 GGRHLIFCHSKKKCDELA AKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG 420

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE

Sbjct 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT

Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT 540

Query 541 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600
 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY

Sbjct 541 HIDAFLSQTQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY 600

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
 RLGAVQNEITLTHP+TKYIMTCMSADLEVVT

Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

> gi|68012726|gb|AAI84759.1| nonstructural protein 3 [Hepatitis C virus]
 Length=631

Score = 1160 bits (3000), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

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Query 1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
Sbjct 1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg 120
Sbjct 61  TRTIASSKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG 120

Query 121  dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
Sbjct 121  D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR 180

Query 181  SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
Sbjct 181  SPVFSNDSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240

Query 241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
Sbjct 241  YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300

Query 301  LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
Sbjct 301  LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK 360

Query 361  GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
Sbjct 361  GGRHLIFCHSKKKKCELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG 420

Query 421  DFDSVIDCNTCVTQTVDfSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE 480
Sbjct 421  DFDSVIDCNTCVTQTVDfSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480

Query 481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
Sbjct 481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540

Query 541  HIDAHLFSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
Sbjct 541  HIDAHLFSQTKQSGENLPY+VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600

Query 601  RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
Sbjct 601  RLGAVQNEITLTHP+TKYIMTCMSADLEVVT 631

```

> [gi|68012712|gb|AA84752.1](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1159 bits (2999), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

```

Query 1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
Sbjct 1  APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61  TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVTRHADVIPVrrrg 120
Sbjct 61  TRTIASSKGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG 120

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Query	121	dsrgsls sprPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DCRGSLLSPRPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA AKLVALG+NAVAYYRGLDVSVIP GDV VVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELA AKLVALGVNAVAYYRGLDVSVIPASGDV VVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631	

> gi|68012752|gb|AAY84772.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012742|gb|AAY84767.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012738|gb|AAY84765.1| nonstructural protein 3 [Hepatitis C virus]
gi|68012728|gb|AAY84760.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1159 bits (2998), Expect = 0.0, Method: Composition-based stats.
Identities = 615/631 (97%), Positives = 622/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsls sprPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DSRGSLLSPRPISYLGSSGGPLLC PAGA HAVGI FRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAA YAAQGYKVLV LNPSVAATLGFGA	

Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKKCELAACKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLFEWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLWAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631	

> [gi|68012708|gb|AA84750.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1159 bits (2997), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSRSLTPCTCGSSDLYLVRHADVIPVrrrg	120
		T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVRHADVIPVRRRG	
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DSRGSLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFSDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360

Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHS KKCDELA AAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSNKKKCELA AAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631	

> gi|68012698|gb|AAY84745.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1159 bits (2997), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTN DQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNGDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLGSSGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFSDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPPAVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKKCELA AAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	

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Sbjct  481  RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT  540

Query  541  HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600
          HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct  541  HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600

Query  601  RLGAQNEITLTHPVTKYIMTCMSADLEVVT  631
          RLGAQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct  601  RLGAQNEITLTHPITKYIMTCMSADLEVVT  631

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> gi|68012714|gb|AA84753.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1158 bits (2996), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

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Query  1      APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG  60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct  1      APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG  60

Query  61      TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg  120
          TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct  61      TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG  120

Query  121     dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR  180
          D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct  121     DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR  180

Query  181     SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA  240
          SPVF+DNSSPP VPQS+QVAHLHA TGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct  181     SPVFSDNSSPPAVPQSYQVAHLHAATGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA  240

Query  241     YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI  300
          YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI
Sbjct  241     YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI  300

Query  301     LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK  360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct  301     LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK  360

Query  361     GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG  420
          GGRHLIFCHSKKKCDELA AKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
Sbjct  361     GGRHLIFCHSKKKCDELA AKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG  420

Query  421     DFDSVIDCNCVTQTVD FSLDPTFTIETITLPQDAVSrtqrngrtgrgKPGIYRFVAPGE  480
          DFDSVIDCNCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE
Sbjct  421     DFDSVIDCNCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE  480

Query  481     RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT  540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Sbjct  481     RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT  540

Query  541     HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600
          HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct  541     HIDAFLSQTQKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY  600

Query  601     RLGAQNEITLTHPVTKYIMTCMSADLEVVT  631
          RLGAQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct  601     RLGAQNEITLTHPITKYIMTCMSADLEVVT  631

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> gi|68012746|gb|AAY84769.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1158 bits (2995), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 622/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFNDNSSPPVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSNDSSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDNFLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDNFLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDNFLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVR+RAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRVRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT	631

> gi|68012744|gb|AAY84768.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1158 bits (2995), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 621/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60

Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	61	T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYL TRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	180
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	181	SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAEATAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAEATAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	360
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	420
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
Sbjct	601	RLGAVQNEITLTHP+TKYIMTCMSADLEVVT 631	

> gi|67810890|gb|AA82031.1| polyprotein [Hepatitis C virus]

Length=1644

Score = 1157 bits (2994), Expect = 0.0, Method: Composition-based stats.
Identities = 598/618 (96%), Positives = 607/618 (98%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	TRTIASPKGPVIQMYTNVD+DLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	DSRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240

Sbjct	1207	SPVFTDNSSPP VPQSFQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTGS ITYST GKFLADGGCSGGAYDIIICDECHS DATSI	300
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSSITYSTCGKFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK L IGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LDIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCD+LA+KLVA+GINAVAYYRG+DVSVIP GDVVVVATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCDLASKLVAMGINAVAYYRGIDVSVIPTSGDVVVVVATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNTCVTQTVDVDFSLDPTFTTIET TLPQDAVSRT+RRGRTGRGKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNTCVTQTVDVDFSLDPTFTTIETTTTLPQDAVSRTRRRGRTGRGKPGIYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	600
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKY 618 RLGAVQNE+ LTHP+TKY	
Sbjct	1627	RLGAVQNEVILTHPITKY 1644	

> [gi|89519419|gb|ABD75831.1|](#) polyprotein [Hepatitis C virus]
Length=3008

Score = 1157 bits (2994), Expect = 0.0, Method: Composition-based stats.
Identities = 598/685 (87%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL IITSLTGRD N+ GEVQ++STA Q+FL T INGV WTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLFSTIIITSLTGRDTNENCGEVQVLSTATQSFLGTAINGVMWTVYHGAG	1086
Query	61	TRTIASPKGPVIMQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVTRHADV+PVRRRG	120
Sbjct	1087	SKTISGPKGPVNQMYTNVDQDLVGWPAPPVKSRLTPCTCGASDLYLVTRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLKGS SGGP L LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+RG+LLS RPIS LKGSSGGP L LCP GHA G+FRAAVCTRGVAKAVDF+PVE+LETTMR	180
Sbjct	1147	DTRGALLSARPISTLKGSSGGP L LCPMGHAAGLFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNS+PP VPQ++QVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSTPPAVPQAYQVAHLHAPTGSKGSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+GIDPNIR+GVRTITTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGIDPNIRSGVRTITTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RLVVLATATPPGSVT PH NIEEVAL TTGE+PFYGKAIPLE+IK	360
Sbjct	1327	LGIGTVLDQAETAGVRLVLATATPPGSVTTPHSNIEEVALPTTGEVFPFYGKAIPLELIK	1386

Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCELA KQLTSLGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	
Sbjct	1447	DFDSVIDCNTSVIQTVDVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1507	RPSGIFDTSVCECYDAGCAWYELTPAETTTTLRAYFNTPGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY	600
		ID HFLSQTKQSGEN PYLVA YQATVCARA APPPSWD MWKCLIRL KPTLHGPTPLLY	
Sbjct	1567	QIDGHFLSQTKQSGENFPYLVA YQATVCARALAPPPSWDTMWKCLIRL KPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
		RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCLS G VVIVGRV	
Sbjct	1627	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLSVGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		VLSG+PAIIPDREVL Y++FDEMEEC	
Sbjct	1687	VLSGQPAIIPDREVL YQQFDEMEEC 1711	

> gi|68012724|gb|AA Y84758.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.
Identities = 613/631 (97%), Positives = 619/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLKGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLKGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLKGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHA TGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAATGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLAT TPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATDTPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA AAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKKCELA AAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480

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Sbjct 421 DFDSVIDCNTCVTQTVDFSLDPTFTTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE 480
          DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE
Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Query 541 HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
          HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct 541 HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
          HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
          RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631
          RLGAVQNEITLTHPITKYIMTCMSADLEVVT

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>gi|68012710|gb|AA84751.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1157 bits (2992), Expect = 0.0, Method: Composition-based stats.
Identities = 614/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

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Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
Sbjct 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
          APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG
Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg 120
          TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG
Sbjct 61 TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG 120
          TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSRLTPCTCGSSDLYLVTRHADVIPVRRRG
Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
          D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
Sbjct 121 DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR 180
          DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR
Query 181 SPVFTDNSSPPVPVQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
          SPVF+DNSSPP VPQS+ VAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Sbjct 181 SPVFSDNSSPPAVPQSYFVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
          SPVFSDNSSPPAVPQSYFVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
Query 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300
          YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI
Sbjct 241 YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI 300
          YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI
Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
          LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
Sbjct 301 LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 360
          LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK
Query 361 GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG 420
          GGRHLIFCHSKKKKCELA AAKLVALG+NAVAYYRGLDVSVIP GDV VVVATDALMTG+TG
Sbjct 361 GGRHLIFCHSKKKKCELA AAKLVALGVNAVAYYRGLDVSVIPASGDV VVVATDALMTGFTG 420
          GGRHLIFCHSKKKKCELA AAKLVALGVNAVAYYRGLDVSVIPASGDV VVVATDALMTGFTG
Query 421 DFDSVIDCNTCVTQTVDFSLDPTFTTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE 480
          DFDSVIDCNTCVTQTVDFSLDPTFTTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE
Sbjct 421 DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480
          DFDSVIDCNTCVTQTVDFSLDPTFTTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE
Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
          RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
Query 541 HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
          HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY
Sbjct 541 HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
          HIDAFLSQTQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY

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Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
 RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
 Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

> gi|68012722|gb|AAV84757.1| nonstructural protein 3 [Hepatitis C virus]
 Length=631

Score = 1156 bits (2991), Expect = 0.0, Method: Composition-based stats.
 Identities = 613/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

Query 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGLLGCIITSLTGRDKNQVEGE+QIVSTAAQTFLATCINGVCWTVYHGAG
 Sbjct 1 APITAYAQQTRGLLGCIITSLTGRDKNQVEGEIQIVSTAAQTFLATCINGVCWTVYHGAG 60

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSALTPTCTCGSSDLYLVTRHADVIPVrrrg 120
 TRTIAS KGPVIQMYTNVDQDLVGWPAPQG+RSALTPTCTCGSSDLYLVTRHADVIPVRRRG
 Sbjct 61 TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPTCTCGSSDLYLVTRHADVIPVRRRG 120

Query 121 dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR
 Sbjct 121 DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR 180

Query 181 SPVFTDNSSPPVVPQS FQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240
 SPVF+DNSSPP VPQS+QVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA
 Sbjct 181 SPVFSDNSSPPAVPQSYQVAHLHAPTSGSKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA 240

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300
 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI
 Sbjct 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI 300

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAGA L VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK
 Sbjct 301 LGIGTVLDQAETAGAILTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK 360

Query 361 GGRHLIFCHSKKKKCELAACKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG 420
 GGRHLIFCHSKKKKCELAACKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG
 Sbjct 361 GGRHLIFCHSKKKKCELAACKLVALGVNAVAYYRGLDVSVIPASGDV VVVATDALMTGFTG 420

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE 480
 DFDSVIDCNTCVTQTVD FSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE
 Sbjct 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE 480

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
 Sbjct 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540

Query 541 HIDAFLSQTQKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY 600
 HIDAFLSQTQKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY
 Sbjct 541 HIDAFLSQTQKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRL KPTLHGPTPLLY 600

Query 601 RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631
 RLGAVQNEITLTHP+TKYIMTCMSADLEVVT
 Sbjct 601 RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631

> gi|68012740|gb|AAV84766.1| nonstructural protein 3 [Hepatitis C virus]
 Length=631

Score = 1155 bits (2989), Expect = 0.0, Method: Composition-based stats.

Identities = 614/631 (97%), Positives = 620/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	61	TRTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLDTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYILKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	121	DSRGSLLSPRPISYILKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETMMR	180
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	181	SPVFSNDSPPAVPVQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTVEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELAACKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	361	GGRHLIFCHSKKKCDELAACKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrrgKPGIYRFVAPGE	480
Sbjct	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETTTTLTPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT	631

> [gi|89519405|gb|ABD75824.1|](#) polyprotein [Hepatitis C virus]
Length=3009

Score = 1155 bits (2987), Expect = 0.0, Method: Composition-based stats.
Identities = 598/685 (87%), Positives = 642/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1028	APITAYAQQTRGL IITSLTGRD N+ GEVQ++STA Q+FL T +NGV WTVYHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1088	++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVTRHADV+PVRRRG	1147

Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1148	D+RG+LLSPRPIS LKGSSGGPLLCP GHA G+FRAAVCTRGVAKAVDF+PVE+LETTMR DTRGALLSPRPIS TLKGSSGGPLLCPMGHAAGLFRAAVCTRGVAKAVDFVPVESLETTMR	1207
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1208	SPVFTDNS+PP VPQ++QVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSTPPAVPQTYQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1268	YMSKA+GIDPNIR+GVRTITTTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I YMSKAYGIDPNIRSGVRTITTTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1328	LGIGTVLDQAETAG RLVLATATPPGSVT PH NIEEVAL TTGE+PFYGKAIPLE+IK LGIGTVLDQAETAGVRLVLATATPPGSVTTPHSNIEEVALPTTGEVPFYGKAIPLELIK	1387
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1388	GGRHLIFCHSKKKCDELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG GGRHLIFCHSKKKCDELA QLTSGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1447
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1448	DFDSVIDCNT V QTVD FSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE DFDSVIDCNTSVIQTVD FSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1508	RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWE VFTGLT RPSGIFDTSVCECYDAGCAWYELTPAETTRLRAYFNTPLPVCQDHLEFWESVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1568	ID HFLSQTKQSGEN PYLVA YQATVCARA APPPSWD MWKCLIRLKP TLHGPTPLLY QIDGHFLSQTKQSGENFPYLVA YQATVCARALAPPPSWDMWKCLIRLKP TLHGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMCMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1628	RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVVLVGGVLAALAAAYCLS G VVIVGRV RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVVLVGGVLAALAAAYCLSVGSVVIVGRV	1687
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1688	VLSG+PAIIPDREVLY++FDEMEEC VLSGQPAIIPDREVLYQQFDEMEEC	1712

> [gi|89519409|gb|ABD75826.1|](#) polyprotein [Hepatitis C virus]
Length=3008

Score = 1154 bits (2984), Expect = 0.0, Method: Composition-based stats.
Identities = 599/685 (87%), Positives = 643/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	AP+TAYAQQTRGL+ IITSLTGRD N+ GEVQ++STA Q+FL T INGV WTVYHGAG APVTAYAQQTRGLVNTIITSLTGRDTNENCGEVQVLSTATQSFLGTAINGVMWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVTRHADV+PVRRRG SKTISGPKGPVNQMYTNVDQDLVGWPAPPGVKS LTPCTCGASDLYLVTRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RG+LLSPRPIS LKGSSGGPLLCP GHA G+FRAAVCTRGVAKAVDFIPVE+L TTMR DTRGALLSPRPIS TLKGSSGGPLLCPMGHAAGLFRAAVCTRGVAKAVDFIPVESLATTTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct		SPVFTDNS+PP VPQ++QVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	

Sbjct	1207	SPVFTDNSTPPAVPQAYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+GIDPNIR+GVRTITTTG+PITYSTY GKFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGIDPNIRSGVRTITTTGAPITYSTY GKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RLVVLATATPPGSVT PH NIEEVAL TTGEIPFYGKAIPLE+IK	
Sbjct	1327	LGIGTVLDQAETAGVRLVVLATATPPGSVTTPHSNIEEVALPTTGEIPFYGKAIPLELIK	1386
Query	361	GGRHLIFCHSKKKKCELA AKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCE+A +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	
Sbjct	1387	GGRHLIFCHSKKKKCEVANQLKSLGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTITETITLPQDAVSrtqrrgrtg rgKPGIYRFVAPGE	480
		DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	
Sbjct	1447	DFDSVIDCNTSVIQTVDFSLDPTFSIETTTIPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSG+FD+SV+CECYDAGCAWYELTPAETT RL RAY NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGIFDTSVIC ECYDAGCAWYELTPAETTTRL RAYFNT PGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTQKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		ID HFLSQTQKQSGEN PYL VAYQATVCARA APPPSWD MWKCLIRLKPTLHGPTPLLY	
Sbjct	1567	QIDGHFLSQTQKQSGENFPYL VAYQATVCARALAPPPSWDTMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	
Sbjct	1627	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSVGSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		VLSG+PAIIPDREVLY++FDEMEEC	
Sbjct	1687	VLSGQPAIIPDREVLYQQFDEMEEC 1711	

> [gi|68012694|gb|AA Y84743.1|](#) nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1153 bits (2983), Expect = 0.0, Method: Composition-based stats.
Identities = 612/631 (96%), Positives = 618/631 (97%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTN DQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNGDQDLVGWPAPQGARS LTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLGSSGGP LLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSNDSPPAVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIR GVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRPGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300

Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLK TLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKTTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631	

> gi|68012696|gb|AA84744.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1153 bits (2982), Expect = 0.0, Method: Composition-based stats.
Identities = 612/631 (96%), Positives = 618/631 (97%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWT YHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTGYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPTCTCGSSDLVLRHADVIPVrrrg	120
		TRTIAS KGPVIQMYTN DQDLVGWPAPQG+RSLTPTCTCGSSDLVLRHADVIPVRRRG	
Sbjct	61	TRTIASSKGPVIQMYTNGDQDLVGWPAPQGARSLTPTCTCGSSDLVLRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D RGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DGRGSLLSPRPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSDNSSPPAVPQSYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIGTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKCDELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	

Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLK TLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKTTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT	631
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT	631

>gi|67810885|gb|AA82029.1| polyprotein [Hepatitis C virus]
Length=1644

Score = 1152 bits (2981), Expect = 0.0, Method: Composition-based stats.
Identities = 599/618 (96%), Positives = 605/618 (97%), Gaps = 0/618 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITSLTGRDKNQ EGEVQIVSTAAQTFLATCINGVCWTVY GAG	
Sbjct	1027	APITAYAQQTRGLLGCIITSLTGRDKNQAEGEVQIVSTAAQTFLATCINGVCWTVYRGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		TRTIASPKGPVIQMYT+VD+DLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	1087	TRTIASPKGPVIQMYTDVDKDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	
Sbjct	1147	DSRGSLSPRPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	1206
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNSSPP VPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFG	
Sbjct	1207	SPVFTDNSSPPAVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGT	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIRTGVRTITTGS ITYSTYGKFLADGGCSGGAYDIIICDECHS DATSI	
Sbjct	1267	YMSKAHGIDPNIRTGVRTITTGSSITYSTYGKFLADGGCSGGAYDIIICDECHSVDATSI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	
Sbjct	1327	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	1386
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA+KLVALGINAVAYYRG+DVSVIP GDVVVVATDALMTGYTG	
Sbjct	1387	GGRHLIFCHSKKKCDELA SKLVALGINAVAYYRGIDVSVIPTSGDVVVVVATDALMTGYTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGK GIYRFVAPGE	
Sbjct	1447	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKLG IYRFVAPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1507	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGEN PYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTL GPTPLLY	
Sbjct	1567	HIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLQGPTPLLY	1626

Query 601 RLGAVQNEITLTHPVTKY 618
 RLGAVQNE+ LTHP+TKY
 Sbjct 1627 RLGAVQNEVILTHPITKY 1644

> gi|89519413|gb|ABD75828.1| polyprotein [Hepatitis C virus]
 Length=3007

Score = 1151 bits (2977), Expect = 0.0, Method: Composition-based stats.
 Identities = 590/685 (86%), Positives = 644/685 (94%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRG+LG IITSLSLTGRD N+ GEVQ++STA Q+FL T INGV WTVYHGAG	
Sbjct	1026	APITAYAQQTRGMLGTIITSLSLTGRDNTNENCGEVQVLSTATQSFGLTAINGVMWTVYHGAG	1085
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg	120
		++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCGSSDL+LVTR+ADV+P+RRRG	
Sbjct	1086	SKTISGPKGPVNQMYTNVDQDLVGWPAPPGVKSLTPCTCGSSDLFLVTRNADVVPPLRRRG	1145
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RG+L+SPRPIS LKSSGGPLLCP GHA GIFRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1146	DTRGALISPRPISTLKSSGGPLLCPGLGHAAGIFRAAVCTRGVAKAVDFVPVESLETTMR	1205
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ++QVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	
Sbjct	1206	SPVFTDNSTPPAVPQTYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1265
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDPNIR+GVRTITTTG+PITYSTY GKFLADGGC+GGAYDIIICDECHSTDAT++	
Sbjct	1266	YMSKAHGIDPNIRSGVRTITTTGAPITYSTY GKFLADGGCAGGAYDIIICDECHSTDATTV	1325
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVT PH NIEEVAL TTGEIPFYGKA IPL ++K	
Sbjct	1326	LGIGTVLDQAETAGARLVVLATATPPGSVTTPHSNIEEVALPTTGEIPFYGKA IPLSLVK	1385
Query	361	GGRHLIFCHSKKKKCEDELA AKLVALGINAVAYYRGLDVSVIP GDVVV ATDALMTGYTG	420
		GGRHLIFCHSKKKKCEDELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	
Sbjct	1386	GGRHLIFCHSKKKKCEDELA QLSSLGLNAVAYYRGLDVSVIP LSGDVVVCATDALMTGFTG	1445
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTTETITLPQDAVSrtqrgrgrgKPGIYRFVAPGE	480
		DFD+VIDCNT V QTVD FSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	
Sbjct	1446	DFDTVIDCNTSVIQTVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1505
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSG+FD+SVLCECYD GCAWYELTPAETT+RLRAY NTPGLPVCQDHLEFWE VFTGLT	
Sbjct	1506	RPSGIFDTSVLCECYDTGCAWYELTPAETTIRLRAYFNT PGLPVCQDHLEFWESVFTGLT	1565
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
		HID HFLSQTKQ+G+N PYL VAYQATVCA+A APPPSWD MWKCL+RLKPTL GPTPLLY	
Sbjct	1566	HIDGHFLSQTKQAGDNFPYL VAYQATVCAKALAPPPSWDTMWKCLLRLKPTLRGPTPLLY	1625
Query	601	RLGAVQNEITLTHPVTKYIMT CMSADLEVVTSTWvlggylaalaaYCLSTGCVVIVGRV	660
		RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWV+VGG+LAALAAAYCLS G VVIVGRV	
Sbjct	1626	RLGSVQNEVT LTHPITKYIMACMSADLEVVTSTWVMVGGLLAALAAAYCLSVGSVVIVGRV	1685
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
		VLSG+PA+IPDREVLY++FDEMEEC	
Sbjct	1686	VLSGQPAVIPDREVLYKQFDEMEEC 1710	

> gi|89519407|gb|ABD75825.1| polyprotein [Hepatitis C virus]

Length=3008

Score = 1151 bits (2977), Expect = 0.0, Method: Composition-based stats.
Identities = 595/685 (86%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1027	APITAYAQQTRGL IITSLTGRD N+ GEVQ++STA Q+FL T +NGV WTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
Sbjct	1087	++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYL+TRHADV+PVRRRG	1146
Query	121	dsrgslsaprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RG+LLSPRP+S LKGSSGGPLLCP GHA G FRAAVCTRGVAKAVDF+PVE+LETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNS+PP VPQ++QVAHLHAPTGSKGSTKVPAAAYA+QGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+GIDPNIR+GVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAG RLVVLATATPPGSVT PH NIEEVAL TTGE+PFYGKAIPLE+IK	1386
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKCELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	1446
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWGVFTGLT	540
Sbjct	1507	RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWE VFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	ID HFLSQTKQSGEN PYLVAQATVCARA APPPSWD MWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWVlvvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685	
Sbjct	1687	VLSG+PAIIPDREVLY++FDEMEEC 1711	

>gi|89519415|gb|ABD75829.1| polyprotein [Hepatitis C virus]
Length=3008

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
Identities = 593/685 (86%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
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Sbjct	1027	APITAYAQQTRGL I+TSLTG+D N+ GEVQ++STA Q+FL T +NGV W+VYHGAG APITAYAQQTRGLFSTIVTSLTGKDTNENCGEVQVLSTATQSFLGTAVNGVMWSVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg ++TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVRHADV+PVRRRG	120
Sbjct	1087	SKTISGPKGPVNQMYTNVDQDLVGWPAPPVKSRLTPCTCGASDLVLRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+RG+LLSPRPIS LKGSSGGPLLCP GHA G+FRAAVCTRGVAKAVDF+PVE+LETTMR	180
Sbjct	1147	DTRGALLSPRPISTLKGSSGGPLLCPMGHAAGLFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFOVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SPVFTDNS+PP VPQ++QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	240
Sbjct	1207	SPVFTDNSTPPAVPQTYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YMSKA+GIDPNIR+GVRTITTG+PITYSTYKFLADGGCSGGAYDIIICDECHSTD+T+I	300
Sbjct	1267	YMSKAYGIDPNIRSGVRTITTGAPITYSTYKFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RL VLATATPPGSVT PH NIEE+AL TTGEIPFYG+AIPL++IK	360
Sbjct	1327	LGIGTVLDQAETAGVRLTVLATATPPGSVTTPHSNIEEIALPTTGEIPFYGRAIPLDLIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKDELA +L ALG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKDELAQLTALGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLPPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	480
Sbjct	1447	DFDSVIDCNTSVIQTVDVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTTRLRAYMNTPLPVCQDHLEFWGVFTGLT RPSG+FD+SVLCECYDAGCAWYELTPAETT RLRAY+NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGIFDTSVLCECYDAGCAWYELTPAETTTRLRAYLNTPLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY ID HFLSQTKQSGEN PYLVAQATVCARA APPPSWD MWKCLIRLKP TLHGPTPLLY	600
Sbjct	1567	QIDGHFLSQTKQSGENFPYLVAQATVCARALAPPPSWDMWKCLIRLKP TLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVI GRV	660
Sbjct	1627	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSVGSVVITGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSG+PAIIPDREVLY++FDEMEEC	
Sbjct	1687	VLSGQPAIIPDREVLYQQFDEMEEC 1711	

>gi|89519411|gb|ABD75827.1| polyprotein [Hepatitis C virus]
Length=2985

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
Identities = 593/685 (86%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL IITSLTGRD N+ GEVQ++STA Q+FL +NGV WTVYHGAG	60
Sbjct	1027	APITAYAQQTRGLFSTIITSLTGRDTNENCGEVQVLSTATQSFLGVAVNGVMWTVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrg ++TI+ PKGP+ QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYL+TRHADV+PVRRRG	120
Sbjct	1087	SKTISGPKGPINQMYTNVDQDLVGWPAPPVKSRLTPCTCGASDLYLITRHADVVPVRRRG	1146

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1147	D+RG+LLSPRPIS LKGSSGGPLLCP GHA GIFRAAVCTRGVAKAVDF+PVE+LETTMR	
		DTRGALLSPRPISTLKSSGGPLLCPMGHAAGIFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1207	SPVF+DNS+PP VPQ++QVAHLHAPTGSKGSTKVPAAAYA QGYKVLVLNPSVAATLGFGA	
		SPVFSDNSTPPAVPQTYQVAHLHAPTGSKGSTKVPAAAYAGQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1267	YMSKA+GIDPNIR+GVRTITTTG+PITYSTYKGFLADGGC GGAYDIIICDECHSTD+T+I	
		YMSKAYGIDPNIRSGVRTITTTGAPITYSTYKGFLADGGCGGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1327	LGIGTVLDQAETAG RLVLATATPPGSVT PH NIEEVAL TTGEIPFYGKAIP++IK	
		LGIGTVLDQAETAGVRLVLATATPPGSVTTPHSNIEEVALPTTGEIPFYGKAIPDLIK	1386
Query	361	GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG	420
Sbjct	1387	GGRHLIFCHSKKKKDELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	
		GGRHLIFCHSKKKKDELAQLSSLGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
Sbjct	1447	DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	
		DFDSVIDCNTSVIQTVDVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1507	RPSG+FD+SVLCECYDAGCAWYELTP+ETT+RLRAY+NTPGLPVCQDHLEFWE VFTGL	
		RPSGIFDTSVLCECYDAGCAWYELTPSETTIRLRLAYLNT PGLPVCQDHLEFWESVFTGLK	1566
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	ID HFLSQTKQSGENLPYLVA YQATVCARA APPPSWD MW+CLIRLKPTLHGPTPLLY	
		QIDGHFLSQTKQSGENLPYLVA YQATVCARALAPPPSWDTMWRCCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
Sbjct	1627	RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	
		RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSVGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1687	VLSG+PAIIPDREVLYR+FDEMEEC	
		VLSGQPAIIPDREVLYRQFDEMEEC	1711

> [gi|81924266|sp|O91936|POLG_HCVSA](#) Genome polyprotein [Contains: Core protein p21 (C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|3660726|gb|AAC61696.1|](#) polyprotein [Hepatitis C virus (isolate SA13)]
 Length=3014

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
 Identities = 585/685 (85%), Positives = 641/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1028	APITAYAQQTRG+LG II SLTGRDKN+ EGEVQ++STA QTFL TCINGV WTV+HGAG	
		APITAYAQQTRGVLGAIIVSLTGRDKN EAGEVQVLSTATQTFLGTCINGVMWTVFHGAG	1087
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+T+A PKGPV+QMYTNVD+DLVGWP P G+RSLTPCTCGS+DLYLVTRHADV+P RRRG	

Sbjct	1088	AKTLAGPKGPVVQMYTNVDKDLVGWPTPPGTRSLTPCTCGSADLYLVTRHADVVPARRRG	1147
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+R SLLSPRPISYLGSSGGP++CP+GH VG+FRAAVCTRGVAKA+DFIPVENLETTMR	
Sbjct	1148	DTRASLLSPRPISYLGSSGGPVMCPSPGHVVGVFRAAVCTRGVAKALDFIPVENLETTMR	1207
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SPVFTDNS+PP VP FQV HLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	
Sbjct	1208	SPVFTDNSTPPAVPHEFQVGHHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	1267
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMS+A+G+DPNIRTGVRT+TTG+ ITYSTYKFLADGGCSGGAYD+IICDECHS DAT+I	
Sbjct	1268	YMSRAYGVDPNIRTGVRTTTGAAITYSTYKFLADGGCSGGAYDVIICDECHSQDATTI	1327
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARLVVLATATPPGSVT PHPNIEEVAL + GEIPFYG+AIPL +IK	
Sbjct	1328	LGIGTVLDQAETAGARLVVLATATPPGSVTTTPHPNIEEVALPSEGEIPFYGRAIPLALIK	1387
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIDGVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA +L + G+NAVAYYRGLDV+VIP GDVVV +TDALMTG+TG	
Sbjct	1388	GGRHLIFCHSKKKKCELAQLTSQGVNAVAYYRGLDVAVIPATGDVVVCSTDALMTGFTG	1447
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNT VTQTVD FSLDPTFTIET T+PQDAVSR+QRRGRTGRG+ GIYR+V+ GE	
Sbjct	1448	DFDSVIDCNTTVTQTVD FSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRHGIYRVSSGE	1507
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSG+FDS VLCECYDAGCAWY+LTPAETTVRLRAY+NTPLPVCQDHLEFWEGVFTGLT	
Sbjct	1508	RPSGIFDSSVLCECYDAGCAWYDLTPAETTVRLRAYLNTPLPVCQDHLEFWEGVFTGLT	1567
Query	541	HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRL KPTLHGPTPLLY	600
		+IDAH LSQTKQ GEN PYLVA YQATVC RA+APPPSWD MWKC++RLKPTL GPTPLLY	
Sbjct	1568	NIDAHMLSQTKQGGENFPYLVA YQATVCVRAKAPPPSWDMWKMLRLKPTLTGPTPLLY	1627
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEITLTHP+TKYIM CMSADLEV+TSTWVLVGGV+AALAAAYCL+ G V IVGR+	
Sbjct	1628	RLGAVQNEITLTHPITKYIMACMSADLEVITSTWVLVGGVVAALAAAYCLTVGSVAIVGRI	1687
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685	
		+LSG+PAIIPDREVL Y++FDEMEEC	
Sbjct	1688	ILSGRPAIIPDREVL YQQFDEMEEC 1712	

>gi|68012734|gb|AA Y84763.1| nonstructural protein 3 [Hepatitis C virus]
Length=631

Score = 1150 bits (2974), Expect = 0.0, Method: Composition-based stats.
Identities = 612/631 (96%), Positives = 619/631 (98%), Gaps = 0/631 (0%)

Query	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	
Sbjct	1	APITAYAQQTRGLLGCIITS LTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrrg	120
		T+TIAS KGPVIQMYTNVDQDLVGWPAPQG+RSLTPCTCGSSDLYLVTRHADVIPVRRRG	
Sbjct	61	TKTIASSKGPVIQMYTNVDQDLVGWPAPQGARSLTPCTCGSSDLYLVTRHADVIPVRRRG	120
Query	121	dsrgsllsprPISYLGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSRGSLSPRPISYLGSSGGPLLCPA HAVGIFRAAVCTRGVAKAVDFIPVE LETTMR	
Sbjct	121	DSRGSLSPRPISYLGSSGGPLLCPAVHAVGIFRAAVCTRGVAKAVDFIPVEGLETTMR	180

Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVF+DNSSPP VPQS+QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	181	SPVFSNDSPPAVPQSYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKAHGIDP IRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	
Sbjct	241	YMSKAHGIDPIIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGI TVLDQAETAGARL VLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLE IK	
Sbjct	301	LGIDTVLDQAETAGARLTVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEAIK	360
Query	361	GGRHLIFCHSKKKKCELAAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELAAKLVALG+NAVAYYRGLDVSVIP GDVVVVATDALMTG+TG	
Sbjct	361	GGRHLIFCHSKKKKCELAAKLVALGVNAVAYYRGLDVSVIPASGDVVVVATDALMTGFTG	420
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLTPQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCNTCVTQTVDFSLDPTFTIET TLPQDAVSRTQRRGRTGRGKPGIYRFV PGE	
Sbjct	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVTPGE	480
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Query	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	
Sbjct	541	HIDAHFLSQTKQSGENLPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVT 631	
		RLGAVQNEITLTHP+TKYIMTCMSADLEVVT	
Sbjct	601	RLGAVQNEITLTHPITKYIMTCMSADLEVVT 631	

>gi|89519417|gb|ABD75830.1| polyprotein [Hepatitis C virus]
Length=3008

Score = 1149 bits (2973), Expect = 0.0, Method: Composition-based stats.
Identities = 594/685 (86%), Positives = 640/685 (93%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGL I+TSLTGRD N+ GEVQ++STA Q+FL T +NGV W+VYHGAG	
Sbjct	1027	APITAYAQQTRGLFSTIVTSLTGRDNTNENCGEVQVLSTATQSFLGTAVNGVMWSVYHGAG	1086
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		+TI+ PKGPV QMYTNVDQDLVGWPAP G +SLTPCTCG+SDLYLVTRHADV+PVRRRG	
Sbjct	1087	GKTISGPKGPVNQMYTNVDQDLVGWPAPPGVKSRLTPCTCGASDLYLVTRHADVVPVRRRG	1146
Query	121	dsrgsllsprPISYLKGSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+RG+LLSPRPIS LKGSSGGPLLCP GH G+FRAAVCTRGVAKAVDF+PVE+LETTMR	
Sbjct	1147	DTRGALLSPRPISLTLKGSSGGPLLCPMGHVAGLFRAAVCTRGVAKAVDFVPVESLETTMR	1206
Query	181	SPVFTDNSSPPVVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SPVFTDNS+PP VPQ++QVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	
Sbjct	1207	SPVFTDNSTPPAVPQTYQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	1266
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YMSKA+GIDPNIR+GVRTITTTG+PITYSTYKGFLADGGCSGGAYDIIICDECHSTD+T+I	
Sbjct	1267	YMSKAYGIDPNIRSGVRTITTTGAPITYSTYKGFLADGGCSGGAYDIIICDECHSTDSTTI	1326
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RLVVLATATPPGSVT PH NIEE+AL TTGEIPFYGKAIPLE+IK	

Sbjct	1327	LGIGTVLDQAETAGVRLVVLATATPPGSVTTPHSNIEEIALPTTGEIPFYGKAIPLELIK	1386
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA +L +LG+NAVAYYRGLDVSVIP GDVVV ATDALMTG+TG	420
Sbjct	1387	GGRHLIFCHSKKKKCELAQQLTSLGLNAVAYYRGLDVSVIPTSGDVVVCATDALMTGFTG	1446
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCNT V QTVDFSLDPTF+IET T+PQDAVSR+QRRGRTGRG+ GIYR+V PGE	480
Sbjct	1447	DFDSVIDCNTSVIQTVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGRLGIYRYVTPGE	1506
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWGVFTGLT RPSG+FD+SV+CECYDAGCAWYELTPAETT RLRAY NTPGLPVCQDHLEFWE VFTGLT	540
Sbjct	1507	RPSGIFDTSVCECYDAGCAWYELTPAETTTTRLRAYFNT PGLPVCQDHLEFWESVFTGLT	1566
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY ID HFLSQTKQSGEN PYL VAYQATVCARA APPPSWD MWKCLIRLKPTLHGPTPLLY	600
Sbjct	1567	QIDGHFLSQTKQSGENFPYL VAYQATVCARALAPPPSWDMWKCLIRLKPTLHGPTPLLY	1626
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLG+VQNE+TLTHP+TKYIM CMSADLEVVTSTWVLVGGVLAALAAAYCLS G VVIVGRV	660
Sbjct	1627	RLGSVQNEVTLTHPITKYIMACMSADLEVVTSTWVLVGGVLAALAAAYCLSVGSSVVIVGRV	1686
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 VLSG+PA+IPDREVLY++FDEMEEC	
Sbjct	1687	VLSGQPAVIPDREVLYQQFDEMEEC 1711	

>[gi|3550759|dbj|BAA32664.1| polyprotein [Hepatitis C virus (isolate Th580)]
gi|81924482|sp|O92529|POLG HCVT5 Genome polyprotein [Contains: Core protein p21 (Caps C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
Length=3019

Score = 1146 bits (2965), Expect = 0.0, Method: Composition-based stats.
Identities = 586/685 (85%), Positives = 633/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL+G I+TSLTGRDKN+ EGEVQ+VSTA Q+FLAT INGV WTVYHGAG	60
Sbjct	1032	APITAYAQQTRGLVGTIVTSLTGRDKN EAGEVQVSTATQSFLATTINGVLWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++ +A PKGPV QMYTNVDQDLVGWPAP G+RSL PCTCGSSDLYLVTR ADVIP RRRG	120
Sbjct	1092	SKNLAGPKGPVCQMYTNVDQDLVGWPAPLGARSLAPCTCGSSDLYLVTRGADVIPARRRG	1151
Query	121	dsrgsllsprPISYLKGS SGGPLLC PAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+R +LLSPRPIS LKGS SGGPL+CP+GH VG+FRAAVCTRGVAKA+DFIPVEN++TTMR	180
Sbjct	1152	DTRAALLSPRPIS TLKGS SGGPLMCPSGHVGLFRAAVCTRGVAKALDFIPVENMDTTMR	1211
Query	181	SPVFTDNSSPPVPVQSFQVAHLHAPT GSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VPQ++QV +LHAPT GSGKST+VPAAYA QGYKVLVLNPSVAATL FGA	240
Sbjct	1212	SPVFTDNSSPPAVPQTYQVGYLHAPT GSGKSTRVPAAYATQGYKVLVLNPSVAATLSFGA	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYGKFLADGGC SGGAYDIIICDECHSTDATSI YMSKAHGIDPNIRTGVRTITTTG P+TYSTYGKFLADGGC SGGAYDIIICDECHSTD T++	300
Sbjct	1272	YMSKAHGIDPNIRTGVRTITTTGGPVTYSTYGKFLADGGC SGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360

Sbjct	1332	LGIGTVLDQAETAG RL VLATATPPGSVTVPHPN I E AL TTGEIPFYGK IPLE IK LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALPTTGEIPFYGKIPLEFIK	1391
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA +L +LG+NAVA+YRG+DV+VIP GDVVV ATDALMTGYTG	420
Sbjct	1392	GGRHLIFCHSKKKKCELSKQLTSLGLNAVAFYRGVDVAVIPTSGDVVVCATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	480
Sbjct	1452	DFDSVIDCNVAVTQVVD FSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDS SVLCECYDAGCAWYELTPAETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFDS VLCE YD GCAWYELTPAETTVRLRAY+NT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1512	RPSGMFDS SVLCEAYDTGCAWYELTPAETTVRLRAYLNT PGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTQKSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQK GEN YLVA YQATVCARA+APPPSWD MWKCL RLKPTL GPTPLLY	600
Sbjct	1572	HIDAHFLSQTQKGGENFAYLVA YQATVCARAKAPPPSWDMWKCLTRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWV+VGGVLAALAAAYCL+ GCVVI GR+	660
Sbjct	1632	RLGAVQNEIVTTHPITKYIMTCMSADLEVITSTWVIVGGVLAALAAAYCLTVGCVVICGRI	1691
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 V SGKPA++PDREVLY++FDEMEEC	
Sbjct	1692	VTSGKPAVVPDREVLYQQFDEMEEC 1716	

>gi|73765377|gb|AAZ85046.1| polyprotein [Hepatitis C virus]
Length=3012

Score = 1145 bits (2961), Expect = 0.0, Method: Composition-based stats.
Identities = 578/685 (84%), Positives = 634/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQT RGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAY QQT RGLLG I+TSLTGRDKN+VEGE+Q+VSTA QTFLAT +NGV WTVYHGAG	60
Sbjct	1034	APITAYHQQT RGLLGTIVTSLTGRDKNVEGEIQVSTATQTFLATAVNGVLWTVYHGAG	1093
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVDQD+VGWPAP G+RSLTPCTCGSSD+YLVTR+ADVIP RRRG	120
Sbjct	1094	SKTLAGPKGPVCQMYTNVDQDMVGWPAPPGARSRLTPCTCGSSDVYLVTRNADVIPARRRG	1153
Query	121	dsrgsllsprPISYLGSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+R LLSPRP+S LKGSSGGP+LCP+GHAVG+FR AAVCTRGVAKA+DF+PVEN+ETTMR	180
Sbjct	1154	DTRAGLLSPRPLSTLKGSSGGPILCPSGHAVGLFR AAVCTRGVAKAIDFVPVENMETTMR	1213
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA SPVFTDNSSPP VP ++QV +LHAPTGS GKSTKVPAAAYA+QGYKVLVLNPSVAATL FG+	240
Sbjct	1214	SPVFTDNSSPPAVPSTYQVGYLHAPTGS GKSTKVPAAAYASQGYKVLVLNPSVAATLAFGS	1273
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTY GKFLADGGCSGGAYDIIICDECHSTDATSI YMSKAHG+DPNIRTGVRTITTTG PITYSTY GKFLADGGCSGGAYDIIICDECHSTD T+I	300
Sbjct	1274	YMSKAHGVDPNIRTGVRTITTTGGPITYSTY GKFLADGGCSGGAYDIIICDECHSTDPTTI	1333
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RL VLATATPPGSVTVPHPN I EVAL TTGE+PFY G+ IPLE IK	360
Sbjct	1334	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNISEVALPTTGEVPPFYGRGIPLEYIK	1393
Query	361	GGRHLIFCHSKKKKCELA AAKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKKCELA +L +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	420
Sbjct	1394	GGRHLIFCHSKKKKCELAQLRSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG	1453

Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1454	DFDSVIDCN VTQ VDFSLDPTFTIET T+PQDAV+R+QRRGRTGRGKPG+YR+V+ GE	1513
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
Sbjct	1514	RPSGFD+ VLCE YD GCAWYELTP+ETTVRLRAY+NTPGLPVCQDHLEFWEGVFTGLT	1573
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY	600
Sbjct	1574	HIDAHFLSQTKQ GEN YLVAYQATVCARA+APPPSWD MWKCL+RLKP L GPTPLLY	1633
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggylaalaayCLSTGCVVIVGRV	660
Sbjct	1634	RLGAVQNE+T THP+TKYIMTCMSADLEV+TS WVL GG+LAALAAAYCL+TG VI GR+	1693
Query	661	VLGKPAIIPDREVLYREFDEMEEC	685
Sbjct	1694	+ SGKPA++PDREVLY++FDEMEEC	1718

> [gi|93102510|gb|ABE98157.1|](#) polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1145 bits (2961), Expect = 0.0, Method: Composition-based stats.
Identities = 581/685 (84%), Positives = 635/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
Sbjct	1032	APITAYAQQTRGL G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTREADVIPVrrrg	120
Sbjct	1092	+RT+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVTREADVIPARRRG	1151
Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
Sbjct	1152	D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DF+PVEN+ETTMR	1211
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA	240
Sbjct	1212	SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA QGYKVLVLNPSVAATL FG+	1271
Query	241	YMSKAHGIDPNIRTVGRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI	300
Sbjct	1272	YM +A+G++PN+RTGVRT+TTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
Sbjct	1332	LGIGTVLDQAE+AG RL VLATATPPGSVTVPHPNI E ALSTTGEIPFYGKAIPLE IK	1391
Query	361	GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
Sbjct	1392	GGRHLIFCHSKKKKDELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITLTPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
Sbjct	1452	DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT	540

Sbjct	1512	RPSGMFDS VLCE YD GCAWYELTP+ETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFDSVVLCEAYDTGCAWYELTPSETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQK GEN YLVAIQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	600
Sbjct	1572	HIDAHFLSQTQKGGENFAYLVAIQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+	660
Sbjct	1632	RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI	1691
Query	661	VLSGKPAIIPDREVLYREFDEMEEC 685 L+GKPA++PDRE+LY++FDEMEEC	
Sbjct	1692	TLTGKPAVVPDREILYQQFDEMEEC 1716	

>gi|93102504|gb|ABE98154.1| polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1144 bits (2958), Expect = 0.0, Method: Composition-based stats.
Identities = 581/685 (84%), Positives = 637/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FL T INGV WTVYHGAG	60
Sbjct	1032	APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLVTSINGVMWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVD+D+VGWP+P G+RSLTPCTCGSSDLYLVTR ADVIP RRRG	120
Sbjct	1092	SKTLAGPKGPVCQMYTNVDKDVVGWPSPPGARSRLTPCTCGSSDLYLVTTREADVIPARRRG	1151
Query	121	dsrgsllsprPISYLKSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FAAVCTRGVAK++DFIPVEN+ETMR	180
Sbjct	1152	DNRAALLSPRPISLTKGSSGGPIMCPSGHVVLGFAAVCTRGVAKSLDFIPVENMETMR	1211
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAYAAQGYKVLVLNPSVAATLGFGA SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA+QGYKVLVLNPSVAATL FG+	240
Sbjct	1212	SPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTRVPAAYASQGYKVLVLNPSVAATLSFGS	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YM +A+G++PNIRTGVRT+TTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++	300
Sbjct	1272	YMRQAYGVEPNIRTGVRTVTTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RL VLATATPPGSVTVPHPN I E ALSTTGEIPFYGKAIPLE IK	360
Sbjct	1332	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALSTTGEIPFYGKAIPLEYIK	1391
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG GGRHLIFCHSKKKCDELA AKL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	420
Sbjct	1392	GGRHLIFCHSKKKCDELA AKLRSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtggrgKPGIYRFVAPGE DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	480
Sbjct	1452	DFDSVIDCNVAVTQVVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT RPSGMFD+ VLCE YD GCAWYELTP+ETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1512	RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY HIDAHFLSQTQK GEN YLVAIQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	600
Sbjct	1572	HIDAHFLSQTQKGGENFAYLVAIQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY	1631


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Query   601   RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV   660
           RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+
Sbjct   1632   RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI   1691

Query   661   VLSGKPAIIPDREVLVREFDEMEEC   685
           L+GKPA++PDRE+LY++FDEMEEC
Sbjct   1692   TLTGKPAVVPDREILYQQFDEMEEC   1716

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> gi|93102494|gb|ABE98149.1| polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1142 bits (2955), Expect = 0.0, Method: Composition-based stats.
Identities = 579/685 (84%), Positives = 636/685 (92%), Gaps = 0/685 (0%)

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Query    1    APITAYAQQTRGLLGCIIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG   60
           APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG
Sbjct   1032   APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSINGVMWTVYHGAG   1091

Query    61    TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLVLRHADVIPVrrrrg   120
           ++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLVLR ADVIP RRRG
Sbjct   1092   SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSLTPCTCGSSDLVLTREADVIPARRRG   1151

Query   121    dsrgsllsprPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR   180
           D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FAAVCTRGVAK++DFIPVEN+ETTMR
Sbjct   1152   DNRAALLSPRPISTLKGSSGGPIMCPSGHVVGLFRAAVCTRGVAKSLDFIPVENMETTMR   1211

Query   181    SPVFTDNSSPPVVPQS FQVAHLHAPTGSGKSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA   240
           SP FTDNS+PP VPQ++QV +LHAPTGSGKST+VPAAYA+QGYKVLVLNPSVAATL FG+
Sbjct   1212   SPSFTDNSTPPAVPQTYQVGYLHAPTGSGKSTRVPAAYASQGYKVLVLNPSVAATLSFGS   1271

Query   241    YMSKAHGIDPNIRTGVRTITTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI   300
           YM +A+G++PN+RTGVRT+TTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++
Sbjct   1272   YMRQAYGVEPNVRTGVRTVTTTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV   1331

Query   301    LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK   360
           LGIGTVLDQAETAG RL VLATATPPGSVTVPHPN I E ALSTTGEIPFYGKAIPLE IK
Sbjct   1332   LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALSTTGEIPFYGKAIPLEYIK   1391

Query   361    GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG   420
           GGRHLIFCHSKKKCDELA +L +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG
Sbjct   1392   GGRHLIFCHSKKKCDELAGQLKSLGNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG   1451

Query   421    DFDSVIDCNTCVTQTVD FSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE   480
           DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRR RTGRGKPG+YR V+ GE
Sbjct   1452   DFDSVIDCNVAVTQVVD FSLDPTFSIETTTVPQDAVSRQRRVRTGRGKPGVYRIVSQGE   1511

Query   481    RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLGPVCQDHLEFWEGVFTGLT   540
           RPSGMFD+ VLCE YD GCAWYELTP+ETTVRLRAYMNTPLGPVCQDHLEFWEGVFTGLT
Sbjct   1512   RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNTPLGPVCQDHLEFWEGVFTGLT   1571

Query   541    HIDAHFLSQTKQSGENLPYLVA YQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY   600
           HIDAHFLSQTKQ GEN YLVA YQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY
Sbjct   1572   HIDAHFLSQTKQGGENFAYLVA YQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY   1631

Query   601    RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvlaalaaYCLSTGCVVIVGRV   660
           RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+
Sbjct   1632   RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI   1691

Query   661    VLSGKPAIIPDREVLVREFDEMEEC   685

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L+GKPA++PDRE+LY++FDEMEEC

Sbjct 1692 TLTGKPAVVPDREILYQQFDEMEEC 1716

> [gi|81985682|sp|Q5I2N3|POLG_HCV6A](#) Genome polyprotein [Contains: Core protein p21 (C) (p21); Core protein p19; Envelope glycoprotein E1 (gp32) (gp35); Envelope glycoprotein E2 (NS1) (gp68) (gp70); p7; Protease NS2-3 (p23); Serine protease/NTPase/helicase NS3 (Hepacivirin) (NS3P) (p70); Nonstructural protein 4A (NS4A) (p8); Nonstructural protein 4B (NS4B) (p27); Nonstructural protein 5A (NS5A) (p56); RNA-directed RNA polymerase (NS5B) (p68)]
[gi|57791994|gb|AAW56714.1|](#) polyprotein [Hepatitis C virus (isolate 6a33)]
 Length=3019

Score = 1142 bits (2955), Expect = 0.0, Method: Composition-based stats.
 Identities = 579/685 (84%), Positives = 637/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG	60
		APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG	
Sbjct	1032	APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSINGVMWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg	120
		++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVTR ADVIP RRRG	
Sbjct	1092	SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSRLTPCTCGSSDLYLVTTREADVIPARRRG	1151
Query	121	dsrgsllsprPISYLGSSSGGPLLCAPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTMR	
Sbjct	1152	DNRAALLSPRPISTLKGSSSGGPVMCPSGHVVLFRFAAVCTRGVAKSLDFIPVENMETTMR	1211
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLPSVAATLGFGA	240
		SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA+QGYKVLVNLPSVAATL FG+	
Sbjct	1212	SPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTRVPAAYASQGYKVLVNLPSVAATLSFGS	1271
Query	241	YMSKAHGIDPNIRTGVRTITTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YM +A+G++PN+RTGVRT+TTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD T++	
Sbjct	1272	YMRQAYGVEPNVRTGVRTVTTGGAITYSTYKGFLADGGCSGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAGARL VLATATPPGS+TVPHPN I E AL TTGEIPFYGKAIPLE IK	
Sbjct	1332	LGIGTVLDQAETAGARLTVLATATPPGSITVPHPNITETALPTTGEIPFYGKAIPLEYIK	1391
Query	361	GGRHLIFCHSKKKCDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKCDELA KL +LG+NAVA+YRG+DVSVIP GDVV+ ATDALMTGYTG	
Sbjct	1392	GGRHLIFCHSKKKCDELAGKLKSLGLNAVAFYRGVDVSVIPTSGDVVICATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTIETITLPQDAVSrtqrrgrtgrgKPGIYRFVAPGE	480
		DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	
Sbjct	1452	DFDSVIDCNVAVTQVVDVDFSLDPTFSIETTTVPQDAVSRQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
		RPSGMFD+ VLCE YD GCAWYELTP+ETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	
Sbjct	1512	RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTKQSGENLPYLVAQATVCARAQAPPPSWDMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ GEN YLVAQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	
Sbjct	1572	HIDAHFLSQTKQGGENFAYLVAQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlvggvlaalaaYCLSTGCVVIVGRV	660
		RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+	
Sbjct	1632	RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI	1691

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 L+GKPA++PDRE+LY++FDEMEEC
 Sbjct 1692 TLTGKPAVVPDREILYQQFDEMEEC 1716

>gi|93102500|gb|ABE98152.1| polyprotein [Hepatitis C virus subtype 6a]
 Length=3019

Score = 1142 bits (2953), Expect = 0.0, Method: Composition-based stats.
 Identities = 582/685 (84%), Positives = 636/685 (92%), Gaps = 0/685 (0%)

Query 1 APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
 APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT +NGV WTVYHGAG
 Sbjct 1032 APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSVNGVMWTVYHGAG 1091

Query 61 TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVRHADVIPVrrrg 120
 ++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVR ADVIP RRRG
 Sbjct 1092 SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSLTPCTCGSSDLYLVTREADVIPARRRG 1151

Query 121 dsrgsllsprPISYLGSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
 D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTMR
 Sbjct 1152 DNRAALLSPRPISTLKGSSGGPIMCPSGHVVGLFRAAVCTRGVAKSLDFIPVENMETTMR 1211

Query 181 SPVFTDNSSPPVVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
 SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA+QGYKVLVNLNPSVAATL FG+
 Sbjct 1212 SPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTRVPAAYASQGYKVLVNLNPSVAATLSFGS 1271

Query 241 YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI 300
 YM +AHG++PNIRTGVRTITTTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++
 Sbjct 1272 YMRQAHGVEPNIRTGVRTITTTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV 1331

Query 301 LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
 LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E AL TTGEIPFYGKAIPLE IK
 Sbjct 1332 LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALPTTGEIPFYGKAIPLEYIK 1391

Query 361 GGRHLIFCHSKKKKDELA AKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
 GGRHLIFCHSKKKKDELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG
 Sbjct 1392 GGRHLIFCHSKKKKDELAGLKLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG 1451

Query 421 DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgKPGIYRFVAPGE 480
 DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE
 Sbjct 1452 DFDSVIDCNVAVTQVDFSLDPTFSIETTTVPQDAVSRQRRGRTGRGKPGVYRFVSQGE 1511

Query 481 RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 540
 RPSGMFD+ VLCE YD GCAWYELTP+ETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT
 Sbjct 1512 RPSGMFDTVLCEAYDTGCAWYELTPSETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLT 1571

Query 541 HIDAFLSQTQKQSGENLPYLVA YQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY 600
 HIDAFLSQTQKQ GEN YLVAYQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY
 Sbjct 1572 HIDAFLSQTQKQGENFAYLVAYQATVCARAKAPPPSWDVMWKCLIRLKPTLTGPTPLLY 1631

Query 601 RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaayCLSTGCVVIVGRV 660
 RLGAVQNEI THP+TKYIMTMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+
 Sbjct 1632 RLGAVQNEIITHPITKYIMTMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI 1691

Query 661 VLSGKPAIIPDREVLRYREFDEMEEC 685
 L+GKPA++PDRE+LY++FDEMEEC
 Sbjct 1692 TLTGKPAVVPDREILYQQFDEMEEC 1716

>gi|93102492|gb|ABE98148.1| polyprotein [Hepatitis C virus subtype 6a]

Length=3019

Score = 1140 bits (2950), Expect = 0.0, Method: Composition-based stats.
Identities = 581/685 (84%), Positives = 637/685 (92%), Gaps = 0/685 (0%)

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Query 1      APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60
              APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG
Sbjct 1032   APITAYAQQTRGLVGTIVTSLTGRDKNQVEGEVQVVSTATQSFLATSINGVMWTVYHGAG 1091

Query 61     TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTREHADVIPVrrrg 120
              ++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYLVTRE ADVIP RRRG
Sbjct 1092   SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSLTPCTCGSSDLYLVTREADVIPARRRG 1151

Query 121    dsrgsllsprPISYLKSSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR 180
              D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTMR
Sbjct 1152   DNRAALLSPRPISLTKGSSSGGPIMCPSGHVVGFLRAAVCTRGVAKSLDFIPVENMETTMR 1211

Query 181    SPVFTDNSSPPVVPQSFQVAHLHAPTGSGBKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA 240
              SP FTDNS+PP VPQ++QV +LHAPTGSGBKST+VPAAYA+QGYKVLVNLNPSVAATL FG+
Sbjct 1212   SPSFTDNSTPPAVPQTYQVGYLHAPTGSBKSTRVPAAYASQGYKVLVNLNPSVAATLSFGS 1271

Query 241    YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI 300
              YM +A+G++PN+RTGVRT+TTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++
Sbjct 1272   YMRQAYGVEPNVRTGVRTVTTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV 1331

Query 301    LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK 360
              LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E ALSTTGEIPFYGKAIPLE IK
Sbjct 1332   LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALSTTGEIPFYGKAIPLEYIK 1391

Query 361    GGRHLIFCHSKKKKDELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG 420
              GGRHLIFCHSKKKKDELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG
Sbjct 1392   GGRHLIFCHSKKKKDELAGKLKSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG 1451

Query 421    DFDSVIDCNTCVTQTVDVDFSLDPTFTIETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE 480
              DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE
Sbjct 1452   DFDSVIDCNVAVTQVVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE 1511

Query 481    RPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 540
              RPSGMFD+ VLCE YD GCAWYELTP+ETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT
Sbjct 1512   RPSGMFDTVVLCAYDTGCAWYELTPSETTVRLRAYMNTPLPVCQDHLEFWEGVFTGLT 1571

Query 541    HIDAHLFSQTKQSGENLPYLVAYQATVCARAQAPPPSWDMWKCLIRLKP TLHGPTPLLY 600
              HIDAHLFSQTKQ GEN YLVAYQATVCARA+APPPSWD MWKCLIRLKP TL GPTPLLY
Sbjct 1572   HIDAHLFSQTKQGENFAYLVAYQATVCARAKAPPPSWDTMWKCLIRLKP TLGTPTPLLY 1631

Query 601    RLGAVQNEITLTHPVTKYIMTCMSADLEVVTSTWvlggvl aalaaYCLSTGCVVIVGRV 660
              RLGAVQNEI THP+TKYIMTCMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+
Sbjct 1632   RLGAVQNEIITTHPITKYIMTCMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI 1691

Query 661    VLSGKPAIIPDREVLRYREFDEMEEC 685
              L+GKPA++PDRE+LY++FDEMEEC
Sbjct 1692   TLTGKPAVVPDREILYQQFDEMEEC 1716

```

>gi|93102502|gb|ABE98153.1| polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1140 bits (2948), Expect = 0.0, Method: Composition-based stats.
Identities = 581/685 (84%), Positives = 636/685 (92%), Gaps = 0/685 (0%)

```

Query 1      APITAYAQQTRGLLGCIITSLSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG 60

```

Sbjct	1032	APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSINGVMWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVD+DLVGWP+P G+RSLTPCTCGSSDLYL+TR ADVIP RRRG	120
Sbjct	1092	SKTLAGPKGPVCQMYTNVDKDLVGWPSPPGARSLTPCTCGSSDLYLITREADVIPARRRG	1151
Query	121	dsrgsllsprPISYLKSSGGPPLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR D+R +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTMR	180
Sbjct	1152	DNRAALLSPRPIS TLKGSSGGPIMCPSGHVVLFRFAAVCTRGVAKSLDFIPVENMETTMR	1211
Query	181	SPVFTDNSSPPVVPQS FQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLVNLNPSVAATLGFGA SP FTDNS+PP VPQ++QV +LHAPTGS GKST+VPAAYA+QGYKVLVNLNPSVAATL FG+	240
Sbjct	1212	SPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTRVPAAYASQGYKVLVNLNPSVAATLSFGS	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKFLADGGCSGGAYDIIICDECHSTDATSI YM +A+G++PNIRTGVRTITTTG ITYSTYKFLADGGCSGGAYDIIICDECHSTD T++	300
Sbjct	1272	YMRQAYGVEPNIRTGVRTITTTGGAITYSTYKFLADGGCSGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E AL TTGEIPFYGKAIPLE IK	360
Sbjct	1332	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALPTTGEIPFYGKAIPLEYIK	1391
Query	361	GGRHLIFCHSKKKCDELA AAKLVALGINAVAYYRGLDVSVIPPIGDV VVVATDALMTGYTG GGRHLIFCHSKKKCDELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	420
Sbjct	1392	GGRHLIFCHSKKKCDELAGKLKSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVD FSLDPTFTIETITL PQDAVSrtqrrgrtgrgKPGIYRFVAPGE DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	480
Sbjct	1452	DFDSVIDCNVAVTQVVD FSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT RPSGMFD+ VLCE YD GCAWYELTP+ETT VRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	540
Sbjct	1512	RPSGMFDTVVLCEAYDTGCAWYELTPSETTVRLRAYMNT PGLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTKQSGENLPYL VAYQATVCARAQAPPPSWDQMWKCLIRLKP TLHGPTPLLY HIDAHFLSQTKQ GEN YLVAYQATVCARA+APPPSWD MWKCLIRLKP TL GPTPLLY	600
Sbjct	1572	HIDAHFLSQTKQSGENFAYLVAYQATVCARAKAPPPSWDIMWKCLIRLKP TLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlvggvl aalaaYCLSTGCVVIVGRV RLGAVQNEI THP+TKYIMTMSADLEV+TSTWVLVGGVLAALAAAYCLS GCVVI GR+	660
Sbjct	1632	RLGAVQNEIITHPITKYIMTMSADLEVITSTWVLVGGVLAALAAAYCLSVGCVVICGRI	1691
Query	661	VLSGKPAIIPDREVL YREFDEMEEC 685 L+GKPA++PDRE+LY++FDEMEEC	
Sbjct	1692	TLTGKPAVVPDREILYQQFDEMEEC 1716	

>gi|93102514|gb|ABE98159.1| polyprotein [Hepatitis C virus subtype 6a]
Length=3019

Score = 1139 bits (2947), Expect = 0.0, Method: Composition-based stats.
Identities = 580/685 (84%), Positives = 635/685 (92%), Gaps = 0/685 (0%)

Query	1	APITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAG APITAYAQQTRGL+G I+TSLTGRDKN+VEGEVQ+VSTA Q+FLAT INGV WTVYHGAG	60
Sbjct	1032	APITAYAQQTRGLVGTIVTSLTGRDKNVEGEVQVVSTATQSFLATSINGVMWTVYHGAG	1091
Query	61	TRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVrrrg ++T+A PKGPV QMYTNVDQDLVGWP+P G+RSLTPCTCGS+DLYLVTR ADVIP RRRG	120
Sbjct	1092	SKTLAGPKGPVCQMYTNVDQDLVGWPSPPGARSLTPCTCGSNDLYLVTRADVIPARRRG	1151

Query	121	dsrgsllsprPISYLKSSGGPLLCPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMR	180
		DSR +LLSPRPIS LKGSSGGP++CP+GH VG+FRAAVCTRGVAK++DFIPVEN+ETTM	
Sbjct	1152	DSRAALLSPRPISLTKGSSGGPIMCPSGHVVGLFRAAVCTRGVAKSLDFIPVENMETTMR	1211
Query	181	SPVFTDNSSPPVVPQSFFQVAHLHAPTGSKGSTKVPAAAYAAQGYKVLVLNPSVAATLGFGA	240
		SP FTDNS+PP VPQ++QV +LHAPTGSKGST+VPAAYA+QGYKVLVLNPSVAATL FG+	
Sbjct	1212	SPSFTDNSTPPAVPQTYQVGYLHAPTGSKGSTRVPAAYASQGYKVLVLNPSVAATLSFGS	1271
Query	241	YMSKAHGIDPNIRTGVRTITTTGSPITYSTYKGFLADGGCSGGAYDIIICDECHSTDATSI	300
		YM +A+G++PN+RTGVRTITTTG ITYSTYKGFLADGGCSGGAYDIIICDECHSTD T++	
Sbjct	1272	YMRQAYGVEPNVRTGVRTITTTGGAITYSTYKGFLADGGCSGGAYDIIICDECHSTDPTTV	1331
Query	301	LGIGTVLDQAETAGARLVVLATATPPGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIK	360
		LGIGTVLDQAETAG RL VLATATPPGSVTVPHPNI E AL TTGEIPFYGKAIPLE IK	
Sbjct	1332	LGIGTVLDQAETAGVRLTVLATATPPGSVTVPHPNITETALPTTGEIPFYGKAIPLEYIK	1391
Query	361	GGRHLIFCHSKKKKCELAALKLVALGINAVAYYRGLDVSVIPPIGDVVVVATDALMTGYTG	420
		GGRHLIFCHSKKKKCELA KL +LG+NAVA+YRG+DVSVIP GDVVV ATDALMTGYTG	
Sbjct	1392	GGRHLIFCHSKKKKCELAGKLKSLGLNAVAFYRGVDVSVIPTSGDVVVCATDALMTGYTG	1451
Query	421	DFDSVIDCNTCVTQTVDFSLDPTFTTETITL PQDAVSrtqrrgrtggrgKPGIYRFVAPGE	480
		DFDSVIDCN VTQ VDFSLDPTF+IET T+PQDAVSR+QRRGRTGRGKPG+YRFV+ GE	
Sbjct	1452	DFDSVIDCNVAVTQVVDVDFSLDPTFSIETTTVPQDAVSRSQRRGRTGRGKPGVYRFVSQGE	1511
Query	481	RPSGMFDSSVLCECYDAGCAWYELTPAETTURLRAYMNTPLPVCQDHLEFWEGVFTGLT	540
		RPSGMFD+ VLCE YD GCAWYELTP+ETTURLRAY+NTPGLPVCQDHLEFWEGVFTGLT	
Sbjct	1512	RPSGMFDTVVLCAYDTGCAWYELTPSETTURLRAYLNTPLPVCQDHLEFWEGVFTGLT	1571
Query	541	HIDAHFLSQTKQSGENLPYLVAIQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLY	600
		HIDAHFLSQTKQ GEN YLVAIQATVCARA+APPPSWD MWKCLIRLKPTL GPTPLLY	
Sbjct	1572	HIDAHFLSQTKQGGENFAYLVAIQATVCARAKAPPPSWDTMWKCLIRLKPTLTGPTPLLY	1631
Query	601	RLGAVQNEITLTHPVTKYIMTMSADLEVVTSTWvlggvlalaaYCLSTGCVVIVGRV	660
		RLGAVQNEI THP+TKYIMTMSADLEV+TSTWV+VGGVLAALAAAYCLS GCVVI GR+	
Sbjct	1632	RLGAVQNEIITTHPITKYIMTMSADLEVITSTWVIVGGVLAALAAAYCLSVGCVVICGRI	1691
Query	661	VLSGKPAIIPDREVLYREFDEMEEC	685
		L+GKP ++PDREVLY++FDEMEEC	
Sbjct	1692	TLTGKPVVVPDREVLYQQFDEMEEC	1716

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Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Jul 20, 2006 3:05 AM

Number of letters in database: 1,312,134,661

Number of sequences in database: 3,805,897

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Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 3805897

Number of Hits to DB: 171000343

Number of extensions: 7142453

Number of successful extensions: 17341
Number of sequences better than 10: 85
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 17304
Number of HSP's successfully gapped: 85
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Length of database: 1312134661
Length adjustment: 137
Effective length of query: 548
Effective length of database: 790726772
Effective search space: 433318271056
Effective search space used: 433318271056
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (20.4 bits)
S2: 80 (35.4 bits)